

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:28:28 / Search time 12.5852 Seconds
(without alignments)
663.334 Million cell updates/sec

Title: US-10-627-141-41

Perfect score: 88
Sequence: 1 ELSGEISAIMRMIGVTGLV 19

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	95.5	19	2	AAW49063 Human Bor
2	81	92.0	370	2	AAW49063 Human Bor
3	48	54.5	358	8	ADN48000 Thermoco
4	47	53.4	300	7	ABO63156 K1ebfiell
5	46	52.3	89	6	ABU06668 Maize Sta
6	46	52.3	89	6	ABU06676 Maize Sta
7	46	52.3	89	6	ABU06669 Maize Sta
8	46	52.3	89	6	ABU06875 Maize Sta
9	46	52.3	89	6	ABU06671 Maize Sta
10	46	52.3	119	6	ABU06221 Maize GBS
11	46	52.3	119	6	ABU06223 Maize GBS
12	46	52.3	119	6	ABU06225 Maize GBS
13	46	52.3	119	6	ABU06229 Maize GBS
14	46	52.3	119	6	ABU06230 Maize GBS
15	46	52.3	119	6	ABU06218 Maize GBS
16	46	52.3	119	6	ABU06219 Maize GBS
17	46	52.3	119	6	ABU06237 Maize GBS
18	46	52.3	119	6	ABU06220 Maize GBS
19	46	52.3	119	6	ABU06239 Maize GBS
20	46	52.3	119	6	ABU06216 Maize GBS
21	46	52.3	119	6	ABU06238 Maize GBS
22	46	52.3	119	6	ABU06232 Maize GBS
23	46	52.3	119	6	ABU06217 Maize GBS
24	46	52.3	119	6	ABU06234 Maize GBS

25	46	52.3	119	6	ABU06236	Abu06236 Maize GBS
26	46	52.3	119	6	ABU06233	Abu06233 Maize GBS
27	46	52.3	119	6	ABU06224	Abu06224 Maize GBS
28	46	52.3	119	6	ABU06215	Abu06215 Maize gra
29	46	52.3	119	6	ABU06227	Abu06227 Maize GBS
30	46	52.3	119	6	ABU06231	Abu06231 Maize GBS
31	46	52.3	119	6	ABU06222	Abu06222 Maize GBS
32	46	52.3	119	6	ABU06226	Abu06226 Maize GBS
33	46	52.3	119	6	ABU06228	Abu06228 Maize GBS
34	46	52.3	185	6	ABU06530	Abu06530 Maize SSI
35	46	52.3	185	6	ABU06531	Abu06531 Maize SSI
36	46	52.3	185	6	ABU06529	Abu06529 Maize SSI
37	46	52.3	468	8	ADX72514	Adx72514 Plant full
38	46	52.3	469	8	ADX88408	Adx88408 Plant full
39	46	52.3	472	8	ADX66065	Adx66065 Plant full
40	46	52.3	533	2	AAW56484	AAW56484 Zea mays
41	46	52.3	574	7	ADF92506	Adf92506 Bread whe
42	46	52.3	600	7	ADM77905	Adm77905 Maize wax
43	46	52.3	600	7	ADM77904	Adm77904 Maize wax
44	46	52.3	604	7	ADF92500	Adf92500 Bread whe
45	46	52.3	604	7	ADF92498	Adf92498 Bread whe

ALIGNMENTS

RESULT 1
AAW49063
ID AAW49063 standard; peptide, 19 AA.
XX
AC AAW49063;
XX
AC
XX
DT 27-AUG-2003 (revised)
DT 09-NOV-1998 (first entry)
XX
DE Human Borna disease virus p40 peptide.
XX
KW BDV, infection; diagnosis; neuropsychiatric disorder; human.
XX
OS Borna disease virus.
XX
PN WO9830238-A1.
XX
PD 16-JUL-1998.
XX
PF 07-JAN-1998; 98WO-US000495.
XX
PR 07-JAN-1997; 97US-00779764.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI De la Torre JC;
XX
DR WPI, 1998-398802/34.
XX
PT New isolated human Borna disease nucleic acid(s) - which encode p24, p16,
PT p36, p40 and L polymerase catalytic domain poly:peptide(s), used to
PT develop products for detection.
XX
PS Claim 5; Page 165; 207pp; English.
XX
CC This peptide is characteristic of novel p40 proteins (see AAW49051-53) of
CC human Borna disease virus (BDV) isolates obtained from psychiatric
CC patients. The invention provides nucleic acids (see AAW32840-55) that
CC encode BDV p24, p16, p36, p40 and L polymerase catalytic domain
CC polypeptides (see AAW49043-63) obtained from psychiatric patients
CC (isolates H1, H2 and H3) as well as from non-human BDV strain V. Also
CC provided are expression vectors, transformed host cells and antibodies
CC raised against the human BDV polypeptides. Human BDV polypeptides,
CC polynucleotides and antibodies can be used in claimed methods for
CC detecting human BDV or human BDV-like viral infection, particularly in
CC patients with neuropsychiatric disorders. (Updated on 27-AUG-2003 to
CC correct OS field.)

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CM protein - protein search, using SW model

Run on: January 17, 2006, 15:55:45 ; Search time 1.25241 seconds
(without alignments)
143.427 Million cell updates/sec

Title: US-10-627-141-41

Perfect score: 88

Sequence: 1 ELSGEISAIKRMIGVTGLV 19

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA New:
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/FCI_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	45.5	286	6	US-10-454-437-78
2	39	44.3	268	7	US-11-082-389-300
3	38	43.2	412	7	US-11-055-822-1086
4	38	43.2	533	6	US-10-467-657-2868
5	37	42.0	253	7	US-11-054-515-1859
6	37	42.0	322	6	US-10-524-647-18
7	37	42.0	565	6	US-10-793-626-2608
8	37	42.0	645	6	US-10-793-626-1770
9	36	40.9	564	6	US-10-517-939-288
10	35.5	40.3	197	7	US-11-082-389-114
11	35	39.8	240	7	US-10-454-437-292
12	35	39.8	259	6	US-10-454-437-292
13	35	39.8	266	7	US-11-055-822-620
14	35	39.8	408	7	US-11-082-389-164
15	35	39.8	760	7	US-11-052-554A-375
16	34.5	39.2	248	6	US-10-467-657-4404
17	34	38.6	48	7	US-11-011-666-8
18	34	38.6	73	6	US-10-485-517-229
19	34	38.6	122	6	US-10-821-234-1638
20	34	38.6	252	6	US-10-467-657-1202
21	34	38.6	254	6	US-11-054-515-1526
22	34	38.6	268	6	US-10-467-657-4064
23	34	38.6	275	7	US-11-065-943-54
24	34	38.6	287	6	US-10-793-626-1146
25	34	38.6	314	6	US-10-485-517-230

26	34	38.6	341	6	US-10-858-730-124	Sequence 124, App
27	34	38.6	376	7	US-11-082-389-122	Sequence 122, App
28	34	38.6	376	7	US-11-082-389-124	Sequence 124, App
29	34	38.6	533	6	US-10-467-657-8	Sequence 8, Appl
30	34	38.6	567	6	US-10-467-657-4328	Sequence 4328, Ap
31	34	38.6	729	7	US-11-210-316-29	Sequence 29, Appl
32	34	38.6	737	7	US-11-210-316-8	Sequence 8, Appl
33	34	38.6	744	7	US-11-052-554A-94	Sequence 94, Appl
34	33.5	38.1	226	6	US-10-878-556A-185	Sequence 185, App
35	33.5	38.1	463	6	US-10-531-844-2	Sequence 2, Appl
36	33	37.5	99	6	US-10-999-866-17	Sequence 17, Appl
37	33	37.5	99	7	US-11-084-554-200	Sequence 200, App
38	33	37.5	99	7	US-11-061-821-17	Sequence 17, Appl
39	33	37.5	109	7	US-11-064-174-61	Sequence 61, Appl
40	33	37.5	114	7	US-11-064-174-62	Sequence 62, Appl
41	33	37.5	119	6	US-10-485-788A-770	Sequence 770, Appl
42	33	37.5	119	7	US-11-053-076-147	Sequence 147, App
43	33	37.5	166	6	US-10-793-626-1576	Sequence 1576, Ap
44	33	37.5	236	6	US-10-793-626-998	Sequence 998, App
45	33	37.5	248	6	US-10-454-437-364	Sequence 364, App

ALIGNMENTS

RESULT 1
US-10-454-437-78
Sequence 78, Application US/10454437
Publication No. US20050277115A1
GENERAL INFORMATION:
APPLICANT: Pompeju, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schröder, Hartwig
APPLICANT: Zeldner, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
FILE REFERENCE: BGI-128CEN
CURRENT FILING DATE: US/10/454,437
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932129.9
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: DE 19932226.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932920.6
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932922.2
PRIOR FILING DATE: 1999-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 442
SEQ ID NO 78
LENGTH: 286
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-10-454-437-78

Query Match 45.5% ; Score 40; DB 6; Length 286;
Best local similarity 50.0% ; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
CY 1 ELSGEISAIKRMIG 14

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:54:39 ; Search time 11.8215 Seconds
(without alignments)
671.550 Million cell updates/sec

Title: US-10-627-141-41

Sequence: 1. ELSGEISAIIRMGVTVGLV 19

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA Main:*

1: /cgn2_6/ptodaca/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodaca/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodaca/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	19	4	US-10-627-141-41
2	46	52.3	89	4	US-10-109-048-574
3	46	52.3	89	4	US-10-109-048-575
4	46	52.3	89	4	US-10-109-048-577
5	46	52.3	89	4	US-10-109-048-577
6	46	52.3	89	4	US-10-109-048-781
7	46	52.3	119	4	US-10-109-048-782
8	46	52.3	119	4	US-10-109-048-121
9	46	52.3	119	4	US-10-109-048-122
10	46	52.3	119	4	US-10-109-048-123
11	46	52.3	119	4	US-10-109-048-124
12	46	52.3	119	4	US-10-109-048-125
13	46	52.3	119	4	US-10-109-048-126
14	46	52.3	119	4	US-10-109-048-128
15	46	52.3	119	4	US-10-109-048-128
16	46	52.3	119	4	US-10-109-048-129
17	46	52.3	119	4	US-10-109-048-130
18	46	52.3	119	4	US-10-109-048-131
19	46	52.3	119	4	US-10-109-048-132
20	46	52.3	119	4	US-10-109-048-133
21	46	52.3	119	4	US-10-109-048-134
22	46	52.3	119	4	US-10-109-048-135
23	46	52.3	119	4	US-10-109-048-136
24	46	52.3	119	4	US-10-109-048-137
25	46	52.3	119	4	US-10-109-048-138
26	46	52.3	119	4	US-10-109-048-139
27	46	52.3	119	4	US-10-109-048-140

28	46	52.3	119	4	US-10-109-048-143	Sequence 143, App
29	46	52.3	119	4	US-10-109-048-144	Sequence 144, App
30	46	52.3	119	4	US-10-109-048-145	Sequence 145, App
31	46	52.3	185	4	US-10-109-048-434	Sequence 434, App
32	46	52.3	185	4	US-10-109-048-435	Sequence 435, App
33	46	52.3	185	4	US-10-109-048-436	Sequence 436, App
34	46	52.3	185	4	US-10-109-048-437	Sequence 437, App
35	46	52.3	185	4	US-10-109-048-437	Sequence 437, App
36	46	52.3	469	4	US-10-425-114-41880	Sequence 41880, A
37	46	52.3	472	4	US-10-425-114-51072	Sequence 51072, A
38	46	52.3	533	4	US-10-628-525-5	Sequence 36908, A
39	46	52.3	591	4	US-10-425-115-339970	Sequence 339970, A
40	46	52.3	600	4	US-10-272-291-3	Sequence 3, Appli
41	46	52.3	600	4	US-10-272-291-4	Sequence 4, Appli
42	46	52.3	604	6	US-11-004-536-4	Sequence 4, Appli
43	46	52.3	604	6	US-11-004-536-6	Sequence 6, Appli
44	46	52.3	605	4	US-10-272-291-6	Sequence 6, Appli
45	46	52.3	605	4	US-10-109-048-34	Sequence 34, Appli

ALIGNMENTS

```
RESULT 1
US-10-627-141-41
; Sequence 41, Application US/10627141
; Publication No. US20040162421A1
; GENERAL INFORMATION:
; APPLICANT: de la Torre, Juan C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
; OF HUMAN BORNA DISEASE VIRUS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10550 North Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: United States
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,141
; FILING DATE: 25-Jul-2003
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,764
; FILING DATE: 16-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 465.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-627-141-41

Query Match 100.0%; Score 88; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:40:34 ; Search time 3.29904 Seconds
(without alignments)
476.151 Million cell updates/sec

Title: US-10-627-141-41

Sequence: 1 ELSGEISAIWMIGVTGLV 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/RB_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	19	2	US-08-779-764A-41
2	88	100.0	19	2	US-09-563-456-41
3	81	92.0	370	2	US-08-369-822C-2
4	81	92.0	370	2	US-08-582-776C-2
5	81	92.0	370	2	US-08-434-831B-2
6	47	53.4	300	2	US-09-489-039A-9673
7	46	52.3	533	2	US-08-941-445A-5
8	46	52.3	604	2	US-09-731-166-4
9	46	52.3	609	2	US-08-941-445A-7
10	45	51.1	820	2	US-09-902-540-16384
11	44	50.0	420	2	US-09-066-047-8
12	43	48.9	89	2	US-09-328-352-5209
13	43	48.9	90	1	US-08-341-219-24
14	43	48.9	90	2	US-08-912-314A-24
15	43	48.9	116	2	US-09-543-681A-6674
16	41.5	47.2	495	2	US-08-984-618-5
17	40	45.5	100	2	US-09-634-955B-29
18	40	45.5	146	2	US-09-583-110-4509
19	40	45.5	168	2	US-08-858-207A-486
20	40	45.5	207	2	US-09-634-955B-28
21	40	45.5	266	2	US-09-602-777A-78
22	40	45.5	365	2	US-09-328-352-7147
23	40	45.5	415	2	US-09-540-236-2213
24	40	45.5	444	2	US-09-861-451A-16
25	39	44.3	59	2	US-09-902-540-13434
26	39	44.3	99	2	US-09-248-796A-18575
27	39	44.3	140	1	US-08-691-071-4

28	39	44.3	140	1	US-08-843-370-4	Sequence 4, Appli
29	39	44.3	157	2	US-10-104-047-3538	Sequence 3538, Ap
30	39	44.3	159	2	US-09-489-039A-12575	Sequence 12575, A
31	39	44.3	308	2	US-09-252-991A-18081	Sequence 18081, A
32	39	44.3	322	2	US-09-107-532A-5708	Sequence 5708, Ap
33	39	44.3	359	1	US-08-976-074-5	Sequence 5, Appli
34	39	44.3	359	1	US-08-083-741-5	Sequence 5, Appli
35	39	44.3	359	2	US-08-976-166A-5	Sequence 5, Appli
36	39	44.3	366	2	US-09-058-725B-4	Sequence 4, Appli
37	39	44.3	386	2	US-09-232-857-4	Sequence 4, Appli
38	39	44.3	409	2	US-09-068-804-42	Sequence 42, Appli
39	39	44.3	410	2	US-09-068-804-6	Sequence 6, Appli
40	39	44.3	512	1	US-08-173-508-4	Sequence 4, Appli
41	39	44.3	512	1	US-08-265-310-4	Sequence 4, Appli
42	39	44.3	512	2	US-08-951-742-4	Sequence 4, Appli
43	39	44.3	512	2	US-09-328-352-5599	Sequence 4, Appli
44	39	43.2	53	2	US-09-621-976-7442	Sequence 5599, Ap
45	38	43.2	53	2	US-09-621-976-7444	Sequence 7442, Ap

ALIGNMENTS

RESULT 1
US-08-779-764A-41
Sequence 41, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPTS RESEARCH INSTITUTE
STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-779-764A-41

Query Match 100.0%; Score 88; DB 2; Length 19;
Best Match Similarity 100.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELSGEISAIWMIGVTGLV 19
|||||
Db 1 ELSGEISAIWMIGVTGLV 19

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 ; Search time 11.3939 Seconds
(without alignments)
1176.511 Million cell updates/sec

Title: US-10-627-141-41
Perfect score: 88
Sequence: 1 ELSGEISAIMRMIGVTGLV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	95.5	370	1 VP40 BDV	Q01552 borna disease
2	84	95.5	370	2 0774E9 BDV	Q074E9 borna disease
3	81	92.0	369	2 0909V1 BDV	Q090V1 borna disease
4	81	92.0	370	2 010392 BDV	Q010392 borna disease
5	81	92.0	370	2 010395 BDV	Q010395 borna disease
6	81	92.0	370	2 010401 BDV	Q010401 borna disease
7	81	92.0	370	2 05GL50 BDV	Q05GL50 borna disease
8	81	92.0	370	2 05GL62 BDV	Q05GL62 borna disease
9	81	92.0	370	2 05GL71 BDV	Q05GL71 borna disease
10	81	92.0	370	2 05GL92 BDV	Q05GL92 borna disease
11	81	92.0	370	2 05GL95 BDV	Q05GL95 borna disease
12	81	92.0	370	2 05GL98 BDV	Q05GL98 borna disease
13	81	92.0	370	2 05GLB3 BDV	Q05GLB3 borna disease
14	81	92.0	370	2 05GLC8 BDV	Q05GLC8 borna disease
15	81	92.0	370	2 08BB29 BDV	Q08BB29 borna disease
16	81	92.0	370	2 0910H1 BDV	Q0910H1 borna disease
17	81	92.0	370	2 091UL4 BDV	Q091UL4 borna disease
18	81	92.0	370	2 091UL8 BDV	Q091UL8 borna disease
19	80	90.9	370	2 010398 BDV	Q010398 borna disease
20	80	90.9	370	2 05GL86 BDV	Q05GL86 borna disease
21	80	90.9	370	2 05GLD1 BDV	Q05GLD1 borna disease
22	48	54.5	123	2 08TMI8 METAC	Q08TMI8 methanobarc
23	48	54.5	256	2 09AME8 PYKOL	Q09AME8 elymus glau
24	48	54.5	358	2 05UDP0 PYKOL	Q05UDP0 pyrococcus
25	47	53.4	188	2 08ZYR2 PYRAB	Q08ZYR2 pyrobaculum
26	47	53.4	254	2 081590 ANOMA	Q081590 anomochloa
27	47	53.4	255	2 081558 9POAL	Q081558 schizachyri
28	47	53.4	373	2 07NIT6 GLOVI	Q07NIT6 gloebacter
29	47	53.4	537	2 0522N2 MAGGR	Q0522N2 magnaportha
30	46	52.3	90	2 0513B4 MORAL	Q0513B4 monopterus
31	46	52.3	244	2 081539 9POAL	Q081539 arundinella

32	46	52.3	246	2	081560 ZEAUT
33	46	52.3	247	2	081596 MELCU
34	46	52.3	248	2	06UTU5 9POAL
35	46	52.3	249	2	06UTU2 TAECM
36	46	52.3	249	2	06UTU7 9POAL
37	46	52.3	249	2	06UTU8 9POAL
38	46	52.3	249	2	06UTV1 9POAL
39	46	52.3	249	2	06UTV2 9POAL
40	46	52.3	249	2	06UTV4 9POAL
41	46	52.3	249	2	06UTV5 9POAL
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43	46	52.3	249	2	06UTV8 9POAL
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					081596 melica cupa
					06utv5 elymus repe
					06utv2 taeniathecu
					06utv7 elymus repe
					06utv8 elymus repe
					06utv1 elymus repe
					06utv2 elymus repe
					06utv4 elymus repe
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					06utv6 elymus repe
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					06utw4 elymus repe

ALIGNMENTS

RESULT 1	ID	VP40 BDV	STANDARD;	PRT;	370 AA.
AC	001552:				
DT	01-JUL-1993 (Rel. 26, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	13-SEP-2005 (Rel. 48, Last annotation update)				
DE	40 kDa protein.				
CN	Name=PA0; Synonyms=P38;				
OS	Borna disease virus (BDV).				
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;				
OC	Bornavirus.				
OX	NCBI_TaxID=12455;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=C6;				
RX	MEDLINE=94149825; PubMed=7906311;				
RA	Cubitt B., Oldstone C., de la Torre J.C.;				
RT	"Sequence and genome organization of Borna disease virus.";				
RL	J. Virol. 68:1382-1396(1994).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.				
RC	STRAIN=Clone B8;				
RX	MEDLINE=93303922; PubMed=8317098;				
RA	Pyper J.M., Richt J.A., Brown L., Rott R., Narayan O., Clements J.B.;				
RT	"Genomic organization of the structural proteins of Borna disease virus revealed by a cDNA clone encoding the 38-kDa protein.";				
RL	Virolgy 195:229-238(1993).				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE OF 10-370.				
RC	STRAIN=Giessen / HR/80-3;				
RA	Birz T., Riehle H., Yamasaki J., Richt J.A., Grebenstein O., Rott R.,				
RT	Niemann H.;				
RL	Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	NUCLEOTIDE SEQUENCE.				
RC	MEDLINE=94207462; PubMed=8254777;				
RX	Schneider P.A., Briese T., Zimmermann W., Ludwig H., Lipkin W.I.;				
RA	"Sequence conservation in field and experimental isolates of Borna disease virus.";				
RL	J. Virol. 68:63-68(1994).				
RN	[5]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=V;				
RX	MEDLINE=94240137; PubMed=8183914;				
RA	Briese T., Schneemann A., Lewis A.J., Park Y.-S., Kim S., Ludwig H.,				
RL	Lipkin W.I.;				
RT	"Genomic organization of Borna disease virus.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 91:4362-4366(1994).				
RN	[6]				
RP	NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.				
RC	STRAIN=HR/80-1;				
RX	MEDLINE=93021385; PubMed=1404604;				

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:55:45 ; Search time 1.1865 Seconds
(without alignments)
143.427 Million cell updates/sec

Title: US-10-627-141-40

Sequence: 1 MEDQDLYEPASLPKLP 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications RA New:*
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3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	42	42.9	1075	6	US-10-821-234-1202	Sequence 1202, App
2	40	40.8	282	6	US-10-972-587-28	Sequence 28, Appl
3	40	40.8	412	6	US-10-524-919-2	Sequence 2, Appl
4	40	40.8	1024	6	US-10-131-826A-198	Sequence 198, Appl
5	39	39.8	798	7	US-11-110-082-39	Sequence 39, Appl
6	38	38.8	358	7	US-11-055-822-572	Sequence 572, App
7	38	38.8	358	7	US-11-055-822-836	Sequence 836, Appl
8	38	38.8	477	7	US-11-055-822-98	Sequence 98, Appl
9	38	38.8	477	7	US-11-186-284-127	Sequence 127, Appl
10	38	38.8	535	6	US-10-793-626-1024	Sequence 1024, App
11	37.5	38.3	406	7	US-11-107-028-7	Sequence 7, Appl
12	37	37.8	132	6	US-10-821-234-1249	Sequence 1249, App
13	37	37.8	151	6	US-10-131-826A-508	Sequence 508, App
14	37	37.8	179	6	US-10-467-657-5942	Sequence 5942, App
15	37	37.8	267	7	US-11-056-408-4	Sequence 4, Appl
16	37	37.8	284	7	US-11-056-408-10	Sequence 10, Appl
17	37	37.8	347	6	US-10-821-234-1379	Sequence 1379, App
18	37	37.8	437	6	US-10-453-372-438	Sequence 438, App
19	37	37.8	633	7	US-11-063-343-26	Sequence 26, App
20	37	37.8	676	6	US-10-453-372-440	Sequence 440, App
21	37	37.8	730	6	US-10-453-372-444	Sequence 444, App
22	37	37.8	737	6	US-10-453-372-434	Sequence 434, App
23	37	37.8	737	6	US-10-453-372-446	Sequence 446, App
24	37	37.8	737	6	US-10-453-372-448	Sequence 448, App
25	37	37.8	737	6	US-10-453-372-450	Sequence 450, App

26	37	737	6	US-10-453-372-452	Sequence 452, App
27	37	737	6	US-10-453-372-454	Sequence 454, App
28	37	737	6	US-10-453-372-456	Sequence 456, App
29	37	378	7	US-11-052-554A-141	Sequence 141, App
30	36	367	7	US-10-845-413-69	Sequence 69, Appl
31	36	367	7	US-10-845-413-70	Sequence 70, Appl
32	36	367	7	US-11-074-176-108	Sequence 108, App
33	36	367	6	US-10-986-501-124	Sequence 124, App
34	36	367	6	US-10-517-939-82	Sequence 82, Appl
35	36	367	6	US-10-524-919-4	Sequence 4, Appl
36	36	367	6	US-11-134-563-16	Sequence 16, Appl
37	36	367	6	US-10-131-826A-544	Sequence 544, App
38	36	367	6	US-10-453-372-260	Sequence 260, App
39	36	367	6	US-10-453-372-258	Sequence 258, App
40	36	367	6	US-10-453-372-266	Sequence 266, App
41	36	367	6	US-10-453-372-280	Sequence 280, App
42	35	357	6	US-10-467-657-2492	Sequence 2492, App
43	35	357	6	US-10-467-657-2496	Sequence 2496, App
44	35	357	7	US-11-102-883-12	Sequence 12, Appl
45	35	357	7	US-11-102-883-36	Sequence 36, Appl

ALIGNMENTS

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RESULT 1
US-10-821-234-1202
; Sequence 1202, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Strache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC SEQ_genes Version 1.0
; SEQ ID NO 1202
; LENGTH: 1075
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1202

Query Match      42.9%; Score 42; DB 6; Length 1075;
Best Local Similarity 53.8%; Pred. NO. 55;
Matches          7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Cy      4 QDDLYEPASLPK 16
Db      391 EDDYSPSKRPK 403

RESULT 2
US-10-972-587-28
; Sequence 28, Application US/10972587
; Publication No. US20050246799A1
; GENERAL INFORMATION:
; APPLICANT: Song, Xiaoling
; APPLICANT: Bartola, Pauline Anne
; APPLICANT: Linderoth, Nora Abiella
; APPLICANT: Fan, Hao
; APPLICANT: Wei, Zhong-Min
; TITLE OF INVENTION: RECEPTORS FOR HYPERSENSITIVE RESPONSE ELICTORS AND
; FILE REFERENCE: 21829/213
; CURRENT APPLICATION NUMBER: US/10/972,587
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: 60/335,776
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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:54:39 ; Search time 11.1994 Seconds
(without alignments)
671.550 Million cell updates/sec

Title: US-10-627-141-40

Sequence: 1 MEDQDLYEPAPLKP 18

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA Main:
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3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	18	US-10-627-141-40	Sequence 40, Appl
2	50	51.0	536	US-11-097-143-7113	Sequence 7113, Ap
3	49	50.0	116	US-10-767-701-50219	Sequence 50219, A
4	49	50.0	630	US-10-259-194A-40	Sequence 40, Appl
5	48	49.0	68	US-10-424-599-215266	Sequence 215266,
6	48	49.0	415	US-10-425-114-48445	Sequence 48445, A
7	48	49.0	456	US-10-437-963-16587	Sequence 16587,
8	47	48.0	68	US-10-681-207-5	Sequence 5, Appl1
9	47	48.0	141	US-10-424-599-151674	Sequence 151674,
10	47	48.0	236	US-10-767-701-40843	Sequence 40843, A
11	47	48.0	623	US-11-097-143-40044	Sequence 40044, A
12	46.5	47.4	357	US-10-282-122A-76274	Sequence 76274, A
13	46	46.9	349	US-10-437-963-162980	Sequence 162980,
14	46	46.9	541	US-10-128-714-8184	Sequence 8184, Ap
15	46	46.9	1369	US-11-097-143-8309	Sequence 9309, Ap
16	46	46.9	6239	US-10-156-761-8477	Sequence 8477, Ap
17	46	46.9	6239	US-10-204-862A-5	Sequence 862A, Ap
18	46	46.9	6239	US-11-005-196-4	Sequence 1964, Appl1
19	45	45.9	429	US-10-437-963-126338	Sequence 126338,
20	45	45.9	474	US-11-097-143-26433	Sequence 26433, A
21	45	45.9	488	US-10-282-122A-51581	Sequence 51581, A
22	45	45.9	700	US-10-282-122A-51105	Sequence 51105, A
23	44	44.9	74	US-11-111-953-725	Sequence 725, Appl
24	44	44.9	105	US-10-424-599-148059	Sequence 148059,
25	44	44.9	193	US-10-767-701-61319	Sequence 61319, A
26	44	44.9	292	US-10-437-963-180963	Sequence 180963,
27	44	44.9	396	US-10-424-599-218884	Sequence 218884,

28	44	44.9	441	US-10-437-963-173638	Sequence 173638,
29	44	44.9	593	US-10-437-963-133881	Sequence 133881,
30	44	44.9	619	US-10-732-923-19401	Sequence 19401, A
31	44	44.9	656	US-10-032-585-7598	Sequence 7598, Ap
32	44	44.9	1028	US-10-369-493-3464	Sequence 3464, Ap
33	44	44.9	3536	US-11-097-143-23232	Sequence 23232, A
34	43.5	44.4	520	US-09-976-782-26	Sequence 26, Appl
35	43	43.9	93	US-10-425-115-278438	Sequence 278438,
36	43	43.9	107	US-10-424-599-215820	Sequence 215820,
37	43	43.9	132	US-10-084-749-2208	Sequence 2208, Ap
38	43	43.9	142	US-10-425-115-214635	Sequence 214635,
39	43	43.9	156	US-10-767-701-32214	Sequence 32214, A
40	43	43.9	160	US-10-424-599-273725	Sequence 273725,
41	43	43.9	189	US-10-425-115-338098	Sequence 338098,
42	43	43.9	203	US-10-282-122A-66541	Sequence 66541, A
43	43	43.9	219	US-10-108-260A-3697	Sequence 3697, Ap
44	43	43.9	222	US-10-739-930-9785	Sequence 9785, Ap
45	43	43.9	258	US-10-408-765A-878	Sequence 878, Appl

ALIGNMENTS

RESULT 1
US-10-627-141-40
Sequence 40, Application US/10627141
Publication No. US20040162421A1
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSER: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 North Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,141
FILING DATE: 25-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-627-141-40
Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDQDLYEPAPLKP 18

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:40:34 ; Search time 3.1254 Seconds
(without alignments)
476.151 Million cell updates/sec

Title: US-10-627-141-40

Perfect score: 98
Sequence: 1 MEDDDLYEPASLPKLP 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	81.5	83.2	370	2	US-08-369-822C-2
4	81.5	83.2	370	2	US-08-582-776C-2
5	81.5	83.2	370	2	US-08-434-831B-2
6	50	51.0	451	2	US-09-248-796A-15169
7	47	48.0	66	2	US-08-945-998A-2
8	46	46.9	153	2	US-09-270-767-33096
9	46	46.9	153	2	US-09-270-767-48313
10	46	46.9	6239	2	US-09-914-286-4
11	44	44.9	501	2	US-09-538-092-707
12	44	44.9	660	2	US-09-248-796A-14578
13	43.5	44.4	465	2	US-09-252-991A-20576
14	43	43.9	320	2	US-09-152-991A-18243
15	42.5	43.4	25	1	US-08-942-423-26
16	42	42.9	72	2	US-09-248-796A-24571
17	42	42.9	744	2	US-09-248-796A-17662
18	42	42.9	806	2	US-09-248-796A-15961
19	42	42.9	2183	2	US-08-746-111-5
20	41	41.8	32	2	US-09-314-268-122
21	41	41.8	47	1	US-08-659-251-37
22	41	41.8	47	1	US-09-256-480-37
23	41	41.8	47	4	PCR-US96-11445-37
24	41	41.8	99	2	US-09-732-210-1583
25	41	41.8	148	2	US-09-248-796A-19533
26	41	41.8	204	2	US-09-540-236-3610
27	41	41.8	311	2	US-09-270-767-33374

28	41	41.8	311	2	US-09-270-767-48591	Sequence 48591, A
29	41	41.8	348	2	US-09-248-528-7	Sequence 7, Appli
30	41	41.8	348	2	US-09-549-108-7	Sequence 7, Appli
31	41	41.8	348	2	US-09-549-111-7	Sequence 7, Appli
32	41	41.8	348	2	US-09-549-106-7	Sequence 7, Appli
33	41	41.8	348	2	US-09-550-394-7	Sequence 14234, A
34	41	41.8	348	2	US-09-902-540-14234	Sequence 105, App
35	41	41.8	434	2	US-09-716-964B-105	Sequence 17104, A
36	41	41.8	446	2	US-09-716-964B-100	Sequence 100, App
37	41	41.8	449	2	US-09-355-214-3	Sequence 3, Appli
38	41	41.8	456	1	US-08-819-013-1	Sequence 1, Appli
39	41	41.8	456	2	US-09-355-214-1	Sequence 1, Appli
40	41	41.8	470	2	US-09-949-016-7976	Sequence 7976, Ap
41	41	41.8	518	2	US-09-902-540-11108	Sequence 11108, A
42	41	41.8	546	2	US-09-252-991A-17104	Sequence 17104, A
43	41	41.8	586	2	US-09-252-991A-29920	Sequence 29920, A
44	41	41.8	2142	2	US-09-538-092-1142	Sequence 1142, Ap
45	41	41.8	2142	2	US-09-949-002-371	Sequence 371, App

ALIGNMENTS

```
RESULT 1
US-08-779-764A-40
; Sequence 40, Application US/08779764A
; Patent No. 6057094
; GENERAL INFORMATION:
; APPLICANT: de la Torre, Juan C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
; TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESS: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: United States
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent'n Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,764A
; FILING DATE: 16-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 465.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-779-764A-40

Query Match 100.0%; Score 98; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEDDDLYEPASLPKLP 18
DB 1 MEDDDLYEPASLPKLP 18
```

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 : Search time 10.7942 Seconds

(without alignments)
1176.511 Million cell updates/sec

Title: US-10-627-141-40

Perfect score: 98
Sequence: 1 MEDDDLYEPASLPKLP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81.5	83.2	370	1 VP40_BDV	O01552 borna disea
2	81.5	83.2	370	2 O10392_BDV	O10392 borna disea
3	81.5	83.2	370	2 O10395_BDV	O10395 borna disea
4	81.5	83.2	370	2 O10398_BDV	O10398 borna disea
5	81.5	83.2	370	2 O10401_BDV	O10401 borna disea
6	81.5	83.2	370	2 O5GL50_BDV	O5GL50 borna disea
7	81.5	83.2	370	2 O5GL71_BDV	O5GL71 borna disea
8	81.5	83.2	370	2 O5GL86_BDV	O5GL86 borna disea
9	81.5	83.2	370	2 O5GL92_BDV	O5GL92 borna disea
10	81.5	83.2	370	2 O5GL98_BDV	O5GL98 borna disea
11	81.5	83.2	370	2 O5GLB3_BDV	O5GLB3 borna disea
12	81.5	83.2	370	2 O8BB29_BDV	O8BB29 borna disea
13	81.5	83.2	370	2 O910H1_BDV	O910H1 borna disea
14	81.5	83.2	370	2 O91UL4_BDV	O91UL4 borna disea
15	81.5	83.2	370	2 O91UL8_BDV	O91UL8 borna disea
16	81.5	83.2	370	2 O774B9_BDV	O774B9 borna disea
17	77.5	79.1	370	2 O5GL62_BDV	O5GL62 borna disea
18	74.5	76.0	370	2 O5GL95_BDV	O5GL95 borna disea
19	74.5	76.0	370	2 O5GLC8_BDV	O5GLC8 borna disea
20	74.5	76.0	370	2 O5GLD1_BDV	O5GLD1 borna disea
21	72.5	74.0	369	2 O9Q9V1_BDV	O9Q9V1 borna disea
22	54	55.1	1408	2 O9M3B9_ARATH	O9M3B9 arabidopsi
23	53	54.1	490	2 O4RNY5_TETNG	O4RNY5 tetradon n
24	53	54.1	722	2 O4WJL3_ASPFU	O4WJL3 aspergillu
25	52	53.1	370	2 O6Y1J3_AANSP	O6Y1J3 anabaena sp
26	52	53.1	1299	2 O623X5_CAEBR	O623X5 caenorhabd
27	51	52.0	201	2 O51066_MAGGR	O51066 magnaporth
28	50	51.0	193	2 O8LGR5_VITVI	O8LGR5 vitis vinif
29	50	51.0	311	2 O9STB4_DROME	O9STB4 drosophila
30	50	51.0	427	2 O5AF05_CANAL	O5AF05 candida alb
31	50	51.0	536	2 O9W0Z3_DROME	O9W0Z3 drosophila

32	50	51.0	850	2 O9W0Z5_DROME	O9W0Z5 drosophila
33	50	51.0	939	2 O5U2Y1_RAT	O5U2Y1 rattus norv
34	49	50.0	303	2 O7GT59_GIALA	O7GT59 giardia lam
35	49	50.0	525	2 O7F0H9_ORISA	O7F0H9 oryza sativ
36	49	50.0	876	2 O60RM3_CAEBR	O60RM3 caenorhabd
37	48.5	49.5	389	2 O5G6S2_9CHIR	O5G6S2 rhyrachomyc
38	48.5	49.5	1055	2 O4RK41_TETNG	O4RK41 tetradon n
39	48	49.0	304	2 O5BKX8_HUMAN	O5BKX8 homo sapien
40	48	49.0	465	2 O523R8_MAGGR	O523R8 magnaporth
41	48	49.0	473	2 O6BPV7_DBBHA	O6BPV7 debaryomyce
42	48	49.0	764	2 O7SFS1_NEUCR	O7SFS1 neurospora
43	48	49.0	858	2 O7SEK3_ASHGO	O7SEK3 ashya gose
44	47.5	48.5	527	2 O5R3Y6_CAEBL	O5R3Y6 caenorhabd
45	47.5	48.5	561	2 O95Q64_CAEBL	O95Q64 caenorhabd

ALIGNMENTS

RESULT 1	VP40_BDV	STANDARD:	PRT:	370 AA.
ID	VP40_BDV			
AC	O01552;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	40 kDa protein.			
GN	Name=P40; Synonyms=P38;			
OS	Borna disease virus (BDV).			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;			
OC	Bornavirus.			
OX	NCBI_Taxid=12455;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=C6;			
RX	MEDLINE=94149825; PubMed=7906311;			
RA	Cubitt B., Oldstone C., de la Torre J.C.;			
RT	"Sequence and genome organization of Borna disease virus.";			
RL	J. Virol. 68:1382-1396(1994).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.			
RC	STRAIN=Clone B8;			
RX	MEDLINE=93303922; PubMed=8317098;			
RT	Pyper J.M., Richt J.A., Brown L., Rott R., Narayan O., Clements J.E.;			
RA	"Genomic organization of the structural proteins of Borna disease			
RT	virus revealed by a cDNA clone encoding the 38-kDa protein.";			
RL	Virology 195:229-238(1993).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE OF 10-370.			
RC	STRAIN=Giesse / HE/80-3;			
RA	Binz T., Riehle H., Yamasaki J., Richt J.A., Grebenstein O., Rott R.,			
RT	Niemann H.;			
RL	Submitted (SEP-1992) to the EMBL/Genbank/DBJ databases.			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=Halle BI/91;			
RX	MEDLINE=94076462; PubMed=8254777;			
RA	Schneider P.A., Briese T., Zimmermann W., Ludwig H., Lipkin W.I.;			
RT	"Sequence conservation in field and experimental isolates of Borna			
RL	disease virus.";			
RL	J. Virol. 68:63-68(1994).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=V;			
RX	MEDLINE=94240137; PubMed=8183914;			
RA	Briese T., Schneemann A., Lewis A.J., Park Y.-S., Kim S., Ludwig H.,			
RT	"Genomic organization of Borna disease virus.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:4362-4366(1994).			
RN	[6]			
RP	NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.			
RC	STRAIN=HE/80-1;			
RX	MEDLINE=93021385; PubMed=1404604;			

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:33:18 ; Search time 1.73633 Seconds
(without alignments)
997.447 Million cell updates/sec

Title: US-10-627-141-40

Perfect score: 98
Sequence: 1 MEDQDLYEPKLP 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81.5	83.2	370	2	A49528
2	54	55.1	1408	2	T47671
3	52	53.1	370	2	AB2490
4	47.5	48.5	721	2	D87753
5	47	48.0	309	2	G87498
6	47	48.0	1743	2	T15893
7	46.5	47.4	357	2	AD1062
8	46	46.9	1545	2	T26589
9	45	45.9	488	2	F97066
10	45	45.9	1217	2	T22672
11	44	44.9	366	2	B84265
12	44	44.9	501	2	B66763
13	44	44.9	533	2	B56110
14	44	44.9	784	2	AP1638
15	43	43.9	116	2	A72641
16	43	43.9	203	2	B83176
17	43	43.9	279	2	H90966
18	43	43.9	279	2	C85832
19	43	43.9	279	2	B64972
20	43	43.9	283	2	G88349
21	43	43.9	283	2	T27027
22	43	43.9	392	1	FOLJGA
23	43	43.9	392	1	FOLJGB
24	43	43.9	393	2	S29356
25	43	43.9	495	2	T00811
26	43	43.9	505	2	T37975
27	43	43.9	510	2	H69893
28	43	43.9	625	2	T16777
29	43	43.9	670	2	T37483

30	43	43.9	903	2	T00358	hypothetical prote
31	43	43.9	1298	2	T47523	DNA-binding protei
32	42.5	43.4	738	2	T27289	hypothetical prote
33	42.5	43.4	1711	2	T11432	hypothetical prote
34	42	42.9	208	2	S00449	photosystem I chal
35	42	42.9	286	2	F87075	membrane transport
36	42	42.9	317	2	S72851	hypothetical prote
37	42	42.9	501	2	T16084	hypothetical prote
38	42	42.9	569	2	B84904	probable lactase
39	42	42.9	623	2	S56206	probable membrane
40	42	42.9	775	2	B64319	carbon-monoxide de
41	42	42.9	957	2	T03829	transcription fact
42	42	42.9	998	2	T09492	general transcript
43	42	42.9	2183	2	T42764	coagulation factor
44	41.5	42.3	992	2	S49835	hypothetical prote
45	41.5	42.3	1225	2	T16346	hypothetical prote

ALIGNMENTS

RESULT 1

probable structural component p40 - Borna disease virus

N.Alternate names: 39k antigen

C.Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000

C.Accession: A49528; A37475; S25642; A44004

R.Schneider, P.A.; Briese, T.; Zimmermann, W.; Ludwig, H.; Lipkin, W.I.

J. Virol. 68, 63-68, 1994

A.Title: Sequence conservation in field and experimental isolates of Borna disease vir

A.Reference number: A49528; MUID:94076462; PMID:8254777

A.Accession: A49528

A.Status: Preliminary

A.Molecule type: genomic RNA

A.Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <DYP>

A.Cross-references: UNIPARC:UPI0000170E05; GB:S62821; NID:9386390; PIDD:AA829214.1; PI

A.Note: sequence extracted from NCBI backbone (NCBIN:141399, NCBIIP:134147)

A.Note: parts of this sequence were confirmed by peptide sequencing

R.Binz, T.; Riehle, H.; Yamasaki, J.; Richt, J.A.; Grebenstein, O.; Rott, R.; Niemann,

submitted to the EMBL Data Library, September 1992

A.Description: The 39/39k antigen of Borna disease virus.

A.Reference number: S25642

A.Accession: S25642

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <BIN>

A.Cross-references: UNIPARC:UPI0000170E05; EMBL:X68392; NID:958687; PIDD:CAA48458.1; P

A.McClure, M.A.; Thibault, R.J.; Hatahaki, C.G.; Lipkin, W.I.

J. Virol. 66, 6572-6577, 1992

A.Title: Sequence similarity between Borna disease virus p40 and a duplicated domain w

A.Reference number: A44004; MUID:93021385; PMID:1404604

A.Accession: A44004

A.Status: preliminary

A.Molecule type: genomic RNA

A.Residues: 14-46, 'I', 48-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <MCC>

A.Cross-references: UNIPARC:UPI0000170E06; GB:M9375; NID:9210698; PIDD:AA73385.1; PI

C.Superfamily: Borna disease virus p40

Query Match 83.2%; Score 81.5; DB 2; Length 370;

Best Local Similarity 94.4%; Pred. No. 4.2e-05;

Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:28:28 ; Search time 11.9228 Seconds
(without alignments)
663.334 Million cell updates/sec

Title: US-10-627-141-40

Perfect score: 98
Sequence: 1 MEDDDLYEPPASLPKLP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	2	AAW49062 Human Bor
2	81.5	83.2	370	2	AAW49062 Human Bor
3	54	55.1	1351	3	AAW49062 Human Bor
4	50	51.0	20	7	AAW49062 Human Bor
5	50	51.0	536	4	AAW49062 Human Bor
6	49	50.0	630	8	AAW49062 Human Bor
7	48	49.0	364	5	AAW49062 Human Bor
8	48	49.0	415	8	AAW49062 Human Bor
9	47	48.0	20	7	AAW49062 Human Bor
10	47	48.0	20	7	AAW49062 Human Bor
11	47	48.0	20	7	AAW49062 Human Bor
12	47	48.0	20	7	AAW49062 Human Bor
13	47	48.0	66	2	AAW49062 Human Bor
14	47	48.0	68	2	AAW49062 Human Bor
15	47	48.0	77	7	AAW49062 Human Bor
16	47	48.0	161	7	AAW49062 Human Bor
17	47	48.0	340	3	AAW49062 Human Bor
18	47	48.0	623	4	AAW49062 Human Bor
19	46.5	47.4	357	6	AAW49062 Human Bor
20	46	46.9	14	7	AAW49062 Human Bor
21	46	46.9	16	7	AAW49062 Human Bor
22	46	46.9	16	7	AAW49062 Human Bor
23	46	46.9	17	7	AAW49062 Human Bor
24	46	46.9	18	7	AAW49062 Human Bor

25	46	46.9	18	7	AAW49062 Human Bor
26	46	46.9	19	7	AAW49062 Human Bor
27	46	46.9	19	7	AAW49062 Human Bor
28	46	46.9	20	7	AAW49062 Human Bor
29	46	46.9	20	7	AAW49062 Human Bor
30	46	46.9	20	7	AAW49062 Human Bor
31	46	46.9	20	7	AAW49062 Human Bor
32	46	46.9	20	7	AAW49062 Human Bor
33	46	46.9	20	7	AAW49062 Human Bor
34	46	46.9	20	7	AAW49062 Human Bor
35	46	46.9	20	7	AAW49062 Human Bor
36	46	46.9	541	6	AAW49062 Human Bor
37	46	46.9	1369	4	AAW49062 Human Bor
38	46	46.9	6239	3	AAW49062 Human Bor
39	46	46.9	6239	4	AAW49062 Human Bor
40	46	46.9	6239	4	AAW49062 Human Bor
41	45	45.9	20	7	AAW49062 Human Bor
42	45	45.9	20	7	AAW49062 Human Bor
43	45	45.9	474	4	AAW49062 Human Bor
44	45	45.9	488	6	AAW49062 Human Bor
45	45	45.9	490	9	AAW49062 Human Bor
46	45	45.9	644	3	AAW49062 Human Bor

ALIGNMENTS

RESULT 1
AAW49062
ID AAW49062 standard; peptide; 18 AA.
XX
AC AAW49062;
XX
DT 27-AUG-2003 (revised)
DT 09-NOV-1998 (first entry)
XX
DE Human Borna disease virus p40 peptide.
XX
KW BDV; infection; diagnosis; neuropsychiatric disorder; human.
XX
OS Borna disease virus.
XX
PN WO9830238-A1.
XX
PD 16-JUL-1998.
XX
PF 07-JAN-1998; 98WO-US000495.
XX
PR 07-JAN-1997; 97US-00779764.
XX
PA (SCRI) SCRIIPS RES INST.
XX
PI De la Torre JC;
XX
DR WPI; 1998-398802/34.
XX
PT New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly:peptide(s), used to develop products for detection.
XX
PS Claim 5; Page 165; 207pp; English.
XX
CC This peptide is characteristic of novel p40 proteins (see AAW49051-53) of human Borna disease virus (BDV) isolates obtained from psychiatric patients. The invention provides nucleic acids (see AAW49051-53) that encode BDV p24, p16, p56, p40 and L polymerase catalytic domain polypeptides (see AAW49043-63) obtained from psychiatric patients (isolates HI, H2 and H3) as well as from non-human BDV strain V. Also provided are expression vectors, transformed host cells and antibodies raised against the human BDV polypeptides. Human BDV polypeptides, polynucleotides and antibodies can be used in claimed methods for detecting human BDV or human BDV-like viral infection, particularly in patients with neuropsychiatric disorders. (Updated on 27-AUG-2003 to correct OS field.)
CC

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:55:45 ; Search time 1.1865 Seconds
(without alignments)
143.427 Million cell updates/sec

Title: US-10-627-141-39

Sequence: 1 MPKRLVDDADAMEDD 18

Scoring table: BLASTSUM62
Gapop 10.0, Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	48.4	156	6 US-10-821-234-939	Sequence 939, App
2	40	42.1	375	7 US-11-051-267-2	Sequence 2, Appli
3	40	42.1	375	7 US-11-051-267-10	Sequence 10, Appl
4	40	42.1	375	7 US-11-051-267-14	Sequence 14, Appl
5	40	42.1	375	7 US-11-051-267-16	Sequence 16, Appl
6	40	42.1	376	7 US-11-051-267-4	Sequence 4, Appli
7	40	42.1	376	7 US-11-051-267-6	Sequence 6, Appli
8	40	42.1	491	6 US-10-954-468-54	Sequence 54, Appl
9	40	42.1	729	6 US-10-954-468-53	Sequence 53, Appl
10	40	42.1	732	6 US-10-954-468-51	Sequence 51, Appl
11	40	42.1	892	6 US-10-507-275-3	Sequence 3, Appli
12	40	42.1	904	6 US-10-507-275-5	Sequence 5, Appli
13	40	42.1	970	6 US-10-087-227-12	Sequence 12, Appl
14	40	42.1	970	6 US-10-954-468-52	Sequence 52, Appl
15	39.5	41.6	229	6 US-10-689-742-38	Sequence 38, Appl
16	39.5	41.6	262	6 US-10-689-742-65	Sequence 65, Appl
17	39	41.1	237	6 US-10-454-437-310	Sequence 310, App
18	39	41.1	421	6 US-10-467-657-5682	Sequence 302, App
19	38	40.0	35	6 US-11-140-930-19	Sequence 19, Appl
20	38	40.0	190	7 US-10-858-730-293	Sequence 293, App
21	38	40.0	540	6 US-10-858-730-293	Sequence 1, Appli
22	38	40.0	747	7 US-11-047-757-1	Sequence 7, Appli
23	38	40.0	747	7 US-11-047-757-1	Sequence 7, Appli
24	37	38.9	3507	7 US-11-075-185-7	Sequence 49, Appl
25	37	38.9	7968	7 US-11-143-980-49	

26	36.5	38.4	317	6 US-10-821-234-1388	Sequence 1388, Ap
27	36.5	38.4	407	6 US-10-821-234-1389	Sequence 1389, Ap
28	36.5	38.4	464	6 US-10-689-742-164	Sequence 164, App
29	36	37.9	15	7 US-11-106-932-53	Sequence 53, Appl
30	36	37.9	31	7 US-11-106-932-3	Sequence 3, Appli
31	36	37.9	222	6 US-10-467-657-20	Sequence 20, Appl
32	36	37.9	222	6 US-10-467-657-6182	Sequence 6182, Ap
33	36	37.9	228	6 US-10-883-512-70	Sequence 70, Appl
34	36	37.9	228	6 US-10-883-512-104	Sequence 104, App
35	36	37.9	228	6 US-10-883-512-104	Sequence 104, App
36	36	37.9	238	6 US-10-467-657-8350	Sequence 8350, App
37	36	37.9	348	6 US-10-467-657-8350	Sequence 20, Appl
38	36	37.9	373	6 US-10-858-730-20	Sequence 8, Appli
39	36	37.9	374	7 US-11-051-267-8	Sequence 18, Appl
40	36	37.9	375	7 US-11-051-267-18	Sequence 1031, Ap
41	36	37.9	399	6 US-10-821-234-1031	Sequence 1536, App
42	36	37.9	417	6 US-10-821-234-1536	Sequence 12, Appl
43	36	37.9	468	7 US-11-054-385-12	Sequence 600, App
44	36	37.9	2261	6 US-10-995-561-600	Sequence 1, Appli
45	36	37.9	2261	6 US-10-511-545-1	

ALIGNMENTS

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RESULT 1
US-10-821-234-939
; Sequence 939, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Scatche-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 939
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-939

Query Match      48.4% Score 46; DB 6; Length 156;
Best Local Similarity 75.0%; Pred. No. 0.71;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      5 RRLVDDADAMED 16
Db      78 RRLVDDTDAMSN 89

RESULT 2
US-11-051-267-2
; Sequence 2, Application US/11051267
; Publication No. US20050257278A1
; GENERAL INFORMATION:
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; FILE REFERENCE: JHU1470-2
; CURRENT APPLICATION NUMBER: US/11/051,267
; CURRENT FILING DATE: 2005-02-03
; PRIOR APPLICATION NUMBER: US/09/841,730
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:54:39 ; Search time 11.1994 Seconds
(without alignments)
671.550 Million cell updates/sec

Title: US-10-627-141-39

Perfect score: 95

Sequence: 1 MPRKRLVDADAMEDD 18

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA Main:

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- 2: /cgn2_6/ptodata/1/pubpa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpa/US10_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	83	87.4	18	US-10-805-220-3	Sequence 3, Appli
3	50	52.6	740	US-10-437-963-196227	Sequence 196227,
4	49	51.6	466	US-10-437-963-136707	Sequence 136707,
5	49	51.6	1011	US-10-437-963-140426	Sequence 140426,
6	48.5	51.1	567	US-10-369-493-22125	Sequence 22125, A
7	48	50.5	707	US-10-425-115-217129	Sequence 217129,
8	48	50.5	736	US-10-425-114-46450	Sequence 46450, A
9	48	50.5	1526	US-10-425-114-65891	Sequence 65891, A
10	48	50.5	1526	US-10-450-763-36475	Sequence 36475, A
11	48	50.5	1554	US-10-450-763-37648	Sequence 37648, A
12	48	50.5	1584	US-10-450-763-37649	Sequence 37649, A
13	48	50.5	1627	US-10-450-763-37649	Sequence 37649, A
14	48	50.5	1881	US-09-998-731-36476	Sequence 36476, A
15	48	50.5	1881	US-09-998-731-36476	Sequence 36476, A
16	48	50.5	1881	US-09-998-731-36476	Sequence 36476, A
17	47	49.5	430	US-10-424-599-166800	Sequence 166800,
18	46	48.4	131	US-09-989-722-276	Sequence 276, App
19	46	48.4	131	US-09-989-723-276	Sequence 276, App
20	46	48.4	131	US-09-989-729-276	Sequence 276, App
21	46	48.4	131	US-09-989-727-276	Sequence 276, App
22	46	48.4	131	US-09-989-731-276	Sequence 276, App
23	46	48.4	131	US-09-989-732-276	Sequence 276, App
24	46	48.4	131	US-09-991-073-276	Sequence 276, App
25	46	48.4	131	US-09-990-442-276	Sequence 276, App
26	46	48.4	131	US-09-991-163-276	Sequence 276, App
27	46	48.4	131	US-09-993-604-276	Sequence 276, App

28	46	48.4	131	US-09-990-456-276	Sequence 276, App
29	46	48.4	131	US-09-989-721-276	Sequence 276, App
30	46	48.4	131	US-09-992-598-276	Sequence 276, App
31	46	48.4	131	US-09-989-293A-276	Sequence 276, App
32	46	48.4	131	US-09-989-735-276	Sequence 276, App
33	46	48.4	131	US-09-990-444-276	Sequence 276, App
34	46	48.4	131	US-09-991-181-276	Sequence 276, App
35	46	48.4	131	US-09-989-730-276	Sequence 276, App
36	46	48.4	131	US-09-990-435-276	Sequence 276, App
37	46	48.4	131	US-09-993-687-276	Sequence 276, App
38	46	48.4	131	US-09-989-734-276	Sequence 276, App
39	46	48.4	131	US-09-997-653-276	Sequence 276, App
40	46	48.4	131	US-09-989-724-276	Sequence 276, App
41	46	48.4	131	US-09-989-728-276	Sequence 276, App
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ALIGNMENTS

RESULT 1
US-10-627-141-39
Sequence 39, Application US/10627141
Publication No. US20040162421A1
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 North Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,141
FILING DATE: 25-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitching, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-627-141-39
Query Match 100.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MPRKRLVDADAMEDD 18

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:40:34 ; Search time 3.1254 Seconds
(without alignment)
476.151 Million cell updates/sec

Title: US-10-627-141-39
Perfect score: 95
Sequence: 1 MPPKRLVDDADAMEDQD 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	95	100.0	18	US-09-563-456-39	Sequence 39, Appl
3	95	100.0	370	US-08-369-822C-2	Sequence 2, Appl
4	95	100.0	370	US-08-582-776C-2	Sequence 2, Appl
5	95	100.0	370	US-08-434-831B-2	Sequence 2, Appl
6	48	50.5	1881	US-09-233-086-3	Sequence 3, Appl
7	46	48.4	131	US-09-839-709-2	Sequence 2, Appl
8	46	48.4	131	US-09-991-181-276	Sequence 276, App
9	46	48.4	131	US-09-990-444-276	Sequence 276, App
10	46	48.4	131	US-09-997-333-276	Sequence 276, App
11	46	48.4	131	US-09-992-598-276	Sequence 276, App
12	43.5	45.8	314	US-08-989-478-4	Sequence 4, Appl
13	43.5	45.8	314	US-08-996-685-4	Sequence 4, Appl
14	41	43.2	41	US-09-314-268-101	Sequence 101, App
15	41	43.2	291	US-09-252-991A-25517	Sequence 25517, A
16	41	43.2	341	US-09-991-181-297	Sequence 297, App
17	41	43.2	341	US-09-990-444-297	Sequence 297, App
18	41	43.2	341	US-09-997-333-297	Sequence 297, App
19	41	43.2	341	US-09-992-598-297	Sequence 297, App
20	41	43.2	342	US-09-252-991A-27223	Sequence 27223, A
21	41	43.2	444	US-09-583-110-2893	Sequence 2893, Ap
22	41	43.2	466	US-09-107-433-3766	Sequence 3766, Ap
23	41	43.2	475	US-10-104-047-2925	Sequence 2925, Ap
24	41	43.2	481	US-09-489-039A-10323	Sequence 10323, A
25	41	43.2	1066	US-09-252-991A-31530	Sequence 31530, A
26	41	43.2	1136	US-09-252-991A-31394	Sequence 31394, A
27	40.5	42.6	1318	US-10-237-551-197	Sequence 197, App

28	40	42.1	70	2	US-09-640-211A-760	Sequence 760, App
29	40	42.1	195	2	US-09-270-767-46801	Sequence 46801, A
30	40	42.1	375	1	US-08-525-596B-14	Sequence 14, Appl
31	40	42.1	375	1	US-08-765-875-5	Sequence 5, Appl
32	40	42.1	375	2	US-08-795-671-5	Sequence 5, Appl
33	40	42.1	375	2	US-09-177-860A-14	Sequence 14, Appl
34	40	42.1	375	2	US-09-252-1498-29	Sequence 29, Appl
35	40	42.1	375	2	US-09-252-1498-30	Sequence 30, Appl
36	40	42.1	375	2	US-09-252-1498-32	Sequence 32, Appl
37	40	42.1	375	2	US-09-252-1498-33	Sequence 33, Appl
38	40	42.1	375	2	US-09-378-238-14	Sequence 14, Appl
39	40	42.1	375	2	US-09-451-501-14	Sequence 14, Appl
40	40	42.1	375	2	US-09-451-501-19	Sequence 19, Appl
41	40	42.1	375	2	US-09-629-938-14	Sequence 14, Appl
42	40	42.1	375	2	US-09-454-540-5	Sequence 5, Appl
43	40	42.1	375	2	US-09-686-344-14	Sequence 14, Appl
44	40	42.1	375	2	US-09-686-344-19	Sequence 19, Appl
45	40	42.1	375	2	US-09-686-344-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-779-764A-39
Sequence 39, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESS: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 NO. 6057094th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-779-764A-39
Query Match 100.0% ; Score 95; DB 2; Length 18;
Best Local Similarity 100.0% ; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPPKRLVDDADAMEDQD 18
Db 1 MPPKRLVDDADAMEDQD 18

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:33:18 ; Search time 1.73633 Seconds
(without alignments)
997.447 Million cell updates/sec

Title: US-10-627-141-39

Perfect score: 95
Sequence: 1 MPPKRLVDDADAMDDQD 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR 80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	43.5	45.8	314	2	A44437
5	43.5	45.8	457	2	S50357
6	43.5	45.8	567	2	S49600
7	43	45.3	302	1	T43822
8	43	45.3	302	2	B84322
9	43	45.3	388	2	AE0421
10	43	45.3	463	2	G45429
11	43	45.3	472	2	T45219
12	43	45.3	790	2	T19683
13	42	44.2	296	2	F70879
14	42	44.2	368	2	T47894
15	42	44.2	425	2	T16433
16	42	44.2	427	2	S19338
17	42	44.2	447	2	T69146
18	42	44.2	559	2	T19444
19	42	44.2	812	2	T34180
20	42	44.2	1287	2	T22235
21	42	44.2	1319	2	S75705
22	41	43.2	266	2	B84292
23	41	43.2	293	2	T22385
24	41	43.2	304	1	R38325
25	41	43.2	411	2	H83355
26	41	43.2	444	2	E95065
27	41	43.2	578	2	T48795
28	41	43.2	754	2	T25551
29	41	43.2	780	2	T37456

30	41	43.2	902	2	T00072	hypothetical prote
31	40	42.1	127	2	T16131	hypothetical prote
32	40	42.1	186	2	T03808	alanine-tRNA ligase
33	40	42.1	223	2	A29770	cerebellar degene
34	40	42.1	307	2	S16622	stage III sporulat
35	40	42.1	414	2	T33878	hypothetical prote
36	40	42.1	469	2	A83411	hypothetical prote
37	40	42.1	469	2	S69640	hypothetical prote
38	40	42.1	501	2	S34825	uvr2 protein - Neu
39	40	42.1	546	2	T32382	hypothetical prote
40	40	42.1	601	2	A82561	hypothetical prote
41	40	42.1	783	2	T37457	Tricorn proteinase
42	40	42.1	799	2	C86287	Pg1.24 protein -
43	40	42.1	830	1	B46723	replication licens
44	40	42.1	868	1	S45757	replication licens
45	40	42.1	881	2	T26498	hypothetical prote

ALIGNMENTS

RESULT 1

A49528 Probable structural component p40 - borna disease virus

N:Alternate names: 39K antigen

C:Species: borna disease virus

C>Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text change 28-Jul-2000

C/Accession: A49528; A37475; S25642; A44004

R/Schneider, P.A.; Brisse, T.; Zimmermann, W.; Ludwig, H.; Lipkin, W.I.

J. Virol. 68, 63-68, 1994

A>Title: Sequence conservation in field and experimental isolates of Borna disease virus

A/Reference number: A49528; PMID:94076462; PMID:8254777

A/Accession: A49528

A>Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 1-370 <SCH>

A/Cross-references: UNIPARC:UPI000017106E; GB:S67502; NID:9456883; PIDD:AA829714.1; PII

A/Experimental source: WT-1, Halle BI/91, horse brain, field isolate

A/Note: sequence extracted from NCBI backbone (NCBIN:141399, NCBIPI:141401)

R/Pyper, J.M.; Richt, J.A.; Brown, L.; Rott, R.; Narayan, O.; Clements, J.E.

Virol. 195, 229-238, 1993

A>Title: Genomic organization of the structural proteins of borna disease virus reveal

A/Reference number: A37475; PMID:93303922; PMID:8317098

A/Accession: A37475

A/Molecule type: mRNA

A/Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <PYP>

A/Cross-references: UNIPARC:UPI0000170E05; GB:S62821; NID:9386390; PIDD:AA827261.1; PII

A/Note: sequence extracted from NCBI backbone (NCBIN:134146, NCBIPI:134147)

R/Blanz, T.; Riehle, H.; Yamasaki, J.; Richt, J.A.; Grebenstein, O.; Rott, R.; Niemann,

submitted to the EMBL Data Library, September 1992

A/Description: The 39/39K antigen of borna disease virus.

A/Reference number: S25642

A/Accession: S25642

A>Status: preliminary

A/Molecule type: mRNA

A/Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <BIN>

A/Cross-references: UNIPARC:UPI0000170E05; EMBL:X68392; NID:958687; PIDD:CAA48458.1; P

R/McClure, W.A.; Thibault, K.J.; Hatala, C.G.; Lipkin, W.I.

J. Virol. 66, 6572-6577, 1992

A>Title: Sequence similarity between Borna disease virus p40 and a duplicated domain w

A/Reference number: A44004; PMID:93021385; PMID:1404604

A/Accession: A44004

A>Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 14-46, 'T', 48-55, 'T', 57-356, 'I', 358-361, 'R', 363-370 <MCC>

A/Cross-references: UNIPARC:UPI0000170E06; GB:M9375; NID:9210698; PIDD:AAA73385.1; P

C/Superfamily: borna disease virus p40

Query Match 100.0%; Score 95; DB 2; Length 370;

Best Local Similarity 100.0%; Pred. No. 3.1e-07; Mismatches 0; Gaps 0;

Matches 18; Conservative 0; Indels 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:55:45 ; Search time 12.4582 Seconds
(without alignments)
143.427 Million cell updates/sec

Title: US-10-627-141-30

Perfect score: 975
Sequence: 1 HTVPSLVFLCLIPGLHAA.....TTIKRYLACMDATLTIPV 189

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76.5	7.8	246	US-11-054-515-1393	Sequence 1393, Ap
2	76.5	7.8	249	US-11-054-515-1347	Sequence 1347, Ap
3	73	7.5	151	US-10-793-626-1646	Sequence 1646, Ap
4	72.5	7.4	1474	US-10-995-561-873	Sequence 873, App
5	70.5	7.2	753	US-10-858-730-225	Sequence 225, App
6	70	7.2	456	US-11-074-176-238	Sequence 238, App
7	68	7.0	181	US-10-467-657-8084	Sequence 8084, Ap
8	67.5	6.9	249	US-11-054-515-1296	Sequence 1296, Ap
9	67.5	6.9	884	US-10-878-556A-9	Sequence 9, Appl
10	67.5	6.9	974	US-10-821-234-1152	Sequence 1152, Ap
11	67	6.9	374	US-10-517-939-356	Sequence 356, Appl
12	67	6.9	1114	US-11-174-150-35	Sequence 35, Appl
13	66.5	6.8	247	US-11-000-463-242	Sequence 242, App
14	66.5	6.8	350	US-11-082-389-380	Sequence 380, App
15	66	6.8	251	US-11-054-515-1669	Sequence 1669, App
16	66	6.8	300	US-10-793-626-1900	Sequence 1900, Ap
17	66	6.8	308	US-10-793-626-1732	Sequence 1732, Ap
18	66	6.8	374	US-10-517-939-340	Sequence 340, App
19	65.5	6.7	442	US-10-467-657-1614	Sequence 1614, App
20	65	6.7	156	US-11-074-176-326	Sequence 326, App
21	65	6.7	172	US-11-074-176-94	Sequence 94, Appl
22	65	6.7	240	US-10-821-234-1003	Sequence 1003, App
23	65	6.7	864	US-11-194-246-343	Sequence 343, App
24	64.5	6.6	210	US-10-793-626-2864	Sequence 2864, Ap
25	64.5	6.6	210	US-10-793-626-3320	Sequence 3320, Ap

26	64	6.6	854	US-10-511-657-4	Sequence 4, Appl
27	63	6.5	232	US-11-055-822-848	Sequence 848, App
28	63	6.5	257	US-11-054-515-1033	Sequence 1033, Ap
29	62.5	6.4	406	US-10-821-234-1521	Sequence 1521, Ap
30	62.5	6.4	572	US-10-454-437-68	Sequence 68, Appl
31	62.5	6.4	584	US-10-454-437-66	Sequence 66, Appl
32	62.5	6.4	795	US-10-821-234-1675	Sequence 1675, Ap
33	62.5	6.4	1141	US-10-601-368-6	Sequence 6, Appl
34	62.5	6.4	1166	US-10-601-368-4	Sequence 4, Appl
35	62.5	6.4	1188	US-10-601-368-3	Sequence 3, Appl
36	62.5	6.4	1188	US-11-000-463-338	Sequence 338, App
37	62.5	6.4	1188	US-11-000-463-810	Sequence 810, App
38	61.5	6.3	391	US-10-613-744-13	Sequence 13, Appl
39	61.5	6.3	623	US-10-873-528-88	Sequence 88, Appl
40	61.5	6.3	993	US-10-055-877-6	Sequence 6, Appl
41	61	6.3	249	US-11-054-515-1445	Sequence 1445, Ap
42	61	6.3	249	US-11-054-515-1641	Sequence 1641, Ap
43	61	6.3	253	US-11-054-515-1242	Sequence 1242, Ap
44	61	6.3	253	US-11-054-515-1298	Sequence 1298, Ap
45	61	6.3	255	US-11-054-515-1281	Sequence 1281, Ap

ALIGNMENTS

RESULT 1
US-11-054-515-1393
Sequence 1393, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P5523P3
CURRENT FILING DATE: 2005-02-10
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1393
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1393
Query Match 7.8%; Score 76.5; DB 7; Length 246;
Best Local Similarity 24.8%; Pred. No. 0.57;
Matches 28; Conservative 19; Mismatches 39; Indels 27; Gaps 7;
CY 86 IKAGAEIKRRKPTMAALRPDSHGRTTLQMPNPHRAIDWT-----NQCPVGSFVLS 140
DB 5 VQSGAR-VKPPGSSVAVSC-KASGQ-----FNSY-AISWQAGQGPENWGRIPIV 54
CY 141 LITDFSPKRFEMDQIKIVASYAQMWTYYTIKE-----YLACMDATL 184

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:54:39 ; Search time 117.593 Seconds
(without alignments)
671.550 Million cell updates/sec

Title: US-10-627-141-30

Perfect score: 975
Sequence: 1 HVTPELVLCILIPGLHAA.....TTIKYIARCMATLTPVY 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	328.5	33.7	273	5	US-10-128-558-370
5	311	31.9	272	5	US-10-128-558-185
6	94.5	9.7	1350	4	US-10-437-963-125423
7	92.5	9.5	940	4	US-10-437-963-197289
8	90	9.2	129	4	US-10-424-599-237276
9	90	9.2	238	4	US-10-291-190-25
10	89.5	9.2	2225	6	US-11-097-143-42423
11	88.5	9.1	1186	4	US-10-437-963-197319
12	87	8.9	270	4	US-10-425-114-56047
13	87	8.9	396	4	US-10-425-114-43995
14	87	8.9	585	4	US-10-424-599-237273
15	85	8.7	82	3	US-09-796-692-2393
16	85	8.7	82	4	US-10-040-862-2393
17	85	8.7	82	4	US-10-057-4758-2393
18	85	8.7	82	4	US-10-154-8848-2393
19	85	8.7	82	4	US-10-764-324-2393
20	85	8.7	1159	4	US-10-437-963-129387
21	84.5	8.6	304	6	US-11-021-619-22
22	83.5	8.6	1959	4	US-10-437-963-154458
23	82.5	8.5	870	4	US-10-437-963-154457
24	81.5	8.4	1190	6	US-11-097-143-14232
25	81.5	8.4	2076	4	US-10-437-963-197291
26	80.5	8.3	1205	4	US-10-437-963-197324
27	79.5	8.2	1278	4	US-10-437-963-181016

28	79	8.1	782	6	US-11-097-143-297	Sequence 297, App
29	78.5	8.1	1389	4	US-10-437-963-129393	Sequence 129393, A
30	78.5	8.1	2393	4	US-10-437-963-197261	Sequence 197261, A
31	78	8.0	620	4	US-10-282-122A-64220	Sequence 64220, A
32	78	8.0	1346	4	US-10-437-963-189131	Sequence 189131, A
33	77.5	7.9	603	4	US-10-425-114-67123	Sequence 67123, A
34	77.5	7.9	609	4	US-10-425-115-274794	Sequence 274794, A
35	77.5	7.9	937	4	US-10-437-963-197334	Sequence 197334, A
36	77.5	7.9	1293	4	US-10-437-963-129354	Sequence 129354, A
37	77	7.9	353	4	US-10-282-122A-74877	Sequence 74877, A
38	77	7.9	420	4	US-10-094-749-2235	Sequence 2235, App
39	77	7.9	481	3	US-09-955-999-104	Sequence 104, App
40	77	7.9	527	4	US-10-437-963-203871	Sequence 203871, A
41	77	7.9	593	5	US-10-732-923-9500	Sequence 9500, App
42	77	7.9	847	4	US-10-478-745-7	Sequence 7, App1
43	76.5	7.8	246	3	US-09-880-748-1393	Sequence 1393, App
44	76.5	7.8	246	4	US-10-293-418-1393	Sequence 1393, App
45	76.5	7.8	249	3	US-09-880-748-1347	Sequence 1347, App

ALIGNMENTS

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US-10-627-141-30
; Sequence 30, Application US/10627141
; Publication No. US20040162421A1
; GENERAL INFORMATION:
; APPLICANT: de la Torre, Juan C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
; OF HUMAN BORNA DISEASE VIRUS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSER: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10550 North Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: United States
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,141
; FILING DATE: 25-Jul-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,764
; FILING DATE: 16-Dec-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Filting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 465.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-627-141-30
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Best Local Similarity 100.0%; Pred. No. 5.5e-102;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 15:40:34 ; Search time 32.8167 Seconds
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476.151 Million cell updates/sec

Title: US-10-627-141-30

Perfect score: 975

Sequence: 1 HTVTPSLVFLCLIPGHAH.....TTIKRYLAECMDATLTIPV 189

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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SUMMARIES

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4	974	99.9	370	2	US-08-582-776C-2
5	974	99.9	370	2	US-08-434-831B-2
6	969	99.4	189	2	US-08-779-764A-28
7	969	99.4	189	2	US-09-563-456-28
8	960	98.5	189	2	US-08-779-764A-29
9	960	98.5	189	2	US-09-563-456-29
10	76.5	7.8	409	2	US-09-270-767-42348
11	76.5	7.8	1919	2	US-10-152-886-13
12	76	7.8	534	1	US-08-577-184-2
13	75	7.7	761	2	US-09-328-352-5650
14	74.5	7.6	519	2	US-09-134-000C-4482
15	74	7.6	470	2	US-09-252-991A-25558
16	73.5	7.5	211	2	US-09-543-681A-6708
17	73.5	7.5	346	2	US-09-724-224-6
18	73.5	7.5	346	2	US-10-093-317-6
19	73.5	7.5	370	2	US-09-724-224-2
20	73.5	7.5	370	2	US-10-093-317-2
21	73.5	7.5	487	2	US-09-724-224-8
22	73.5	7.5	487	2	US-10-093-317-8
23	73.5	7.5	490	2	US-09-949-016-8784
24	73.5	7.5	512	2	US-09-724-224-4
25	73.5	7.5	512	2	US-10-093-317-4
26	73.5	7.5	568	2	US-09-489-039A-13755
27	73.5	7.5	665	2	US-09-595-684B-35

28	73.5	7.5	859	2	US-09-902-540-14220	Sequence 14220, A
29	73	7.5	151	2	US-09-710-279-1646	Sequence 1646, Ap
30	73	7.5	154	2	US-09-134-001C-4123	Sequence 4123, Ap
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33	72.5	7.4	1474	2	US-09-949-002-287	Sequence 287, App
34	72.5	7.4	1491	2	US-09-949-002-434	Sequence 434, Appl
35	72	7.4	440	2	US-09-591-095-27	Sequence 27, Appl
36	72	7.4	488	2	US-09-540-236-3027	Sequence 3027, Ap
37	72	7.4	1695	2	US-09-866-108A-15753	Sequence 15753, A
38	71.5	7.3	427	2	US-09-469-039A-12852	Sequence 12852, A
39	71	7.3	946	4	PCT-US95-08493-13	Sequence 13, Appl
40	71	7.3	2522	2	US-09-251-645-13	Sequence 13, Appl
41	70.5	7.2	387	1	US-08-123-161A-10	Sequence 10, Appl
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ALIGNMENTS

RESULT 1
US-08-779-764A-30
Sequence 30, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSER: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 NO. 6057094th Torrey Pine Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2837
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-764A-30
Query Match 100.0%; Score 975; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 6.2e-111;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 HTVTPSLVFLCLIPGHAHFGVGVRESYLSPTIRGEQTVVKTAKFYGEKTDQDLT 60
QY 61 ELHISFISGCGLLIGVIGSSSKIKAGKQIKKPKTKMALNPSHETATLQWEN 120

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:33:18 ; Search time 18.2315 Seconds
(without alignments)
997.447 Million cell updates/sec

Title: US-10-627-141-30

Perfect score: 975

Sequence: 1 HTVPSLVFCLTIPGHAA.....TTIKVLAECMDATITIPV 189

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Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	974	99.9	370	A49528	probable structural
2	86	8.8	448	A11659	DNA repair protein
3	81.5	8.4	200	C41873	heat shock protein
4	81.5	8.4	200	A97058	molecular chaperon
5	79	8.1	1021	T42634	connectin/chaperon
6	78.5	8.1	352	A69743	ATP-binding Mrp-11
7	78	8.0	620	S73809	DNA primase - Myco
8	76.5	7.8	337	A10061	hypothetical prote
9	76.5	7.8	350	AC0813	ethanolamine opero
10	76.5	7.8	592	E75032	carbon starvation
11	76	7.8	408	T32237	hypothetical prote
12	76	7.8	433	S05654	ND3 function protein
13	76	7.8	843	S77217	phosphorylase (EC
14	76	7.8	2123	S55089	probable acetyl-Co
15	75.5	7.7	389	SYPCF	naringenin-chalcon
16	75.5	7.7	493	C71903	D-alanyl-D-alanine
17	75	7.7	1252	B42771	reticulocyte-bind
18	74.5	7.6	311	AH2153	hypothetical prote
19	74.5	7.6	329	H71192	hypothetical prote
20	74.5	7.6	457	G82187	biopolymer transpo
21	74	7.6	427	D83347	probable aminotran
22	74	7.6	500	T19545	hypothetical prote
23	73.5	7.5	274	C72236	phosphate ABC tran
24	73.5	7.5	383	H86232	hypothetical prote
25	73.5	7.5	920	T11052	antipeptidase (EC
26	73	7.5	233	B61222	cytochrome-c oxida
27	73	7.5	388	T36766	probable two-compo
28	73	7.5	507	B89792	hypothetical prote
29	73	7.5	908	S51293	probable membrane

30	72.5	7.4	330	2	T49002	hypothetical prote
31	72.5	7.4	662	2	C54078	methyl-accepting c
32	72.5	7.4	753	2	B86078	terranhydropteroyl
33	72.5	7.4	753	2	G91223	alpha-2-macroglobu
34	72.5	7.4	1474	1	MAHU	polyprotein - echo
35	72.5	7.4	2180	2	A46182	probable lact-fam
36	72	7.4	335	2	AB0983	hypothetical prote
37	72	7.4	351	2	T29369	penicillin-binding
38	72	7.4	666	2	S54401	probable glycosyl
39	72	7.4	678	2	AE0948	hypothetical prote
40	72	7.4	1224	2	T19749	ABC transporter (A
41	72	7.4	1333	2	S65812	ATP-dependent heli
42	71.5	7.3	300	2	AE1723	hypothetical prote
43	71.5	7.3	708	2	H82751	hypothetical prote
44	71.5	7.3	803	2	T00092	hypothetical prote
45	71.5	7.3	857	2	C97707	clpB protein [limpo

ALIGNMENTS

RESULT 1

A49528

probable structural component p40 - borna disease virus

N/Alternate names: 39K antigen

C/Species: borna disease virus

C/Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text change 28-Jul-2000

C/Accession: A49528; A37475; S25642; A44004

R/Schneider, P.A.; Brisse, T.; Zimmermann, W.; Ludwig, H.; Lipkin, W.I.

J. Virol. 68, 63-68, 1994

A/Title: Sequence conservation in field and experimental isolates of Borna disease virus

A/Reference number: A49528; MUID:94076462; PMID:8254777

A/Accession: A49528

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 1-370 <SCG>

A/Cross-references: UNIPARC:UPI000017106R; GB:S67502; NID:G456883; PIND:AB27261.1; PI

A/Experimental source: WT-1, Halle BI/91, horse brain, field isolate

R/Pyper, J.M.; Richt, J.A.; Brown, L.; Rott, R.; Narayan, O.; Clements, J.R.

Virol. 195, 229-238, 1993

A/Title: Genomic organization of the structural proteins of borna disease virus reveal

A/Reference number: A37475; MUID:93303922; PMID:8317098

A/Accession: A37475

A/Molecule type: RNA

A/Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <PYP>

A/Cross-references: UNIPARC:UPI0000170B05; GB:S62821; NID:G386390; PIND:AB27261.1; PI

A/Note: sequence extracted from NCBI backbone (NCBIN:134146, NCBI:P.134147)

A/Note: parts of this sequence were confirmed by peptide sequencing

R/Blinz, T.; Riehle, H.; Yamasaki, J.; Richt, J.A.; Grebenstein, O.; Rott, R.; Niemann,

submitted to the EMBL Data Library, September 1992

A/Description: The 39/39K antigen of borna disease virus.

A/Reference number: S25642

A/Accession: S25642

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <BIN>

A/Cross-references: UNIPARC:UPI0000170B05; EMBL:X68392; NID:G58687; PIND:CAA48458.1; P

R/McClure, M.A.; Thibault, K.J.; Hattalaki, C.G.; Lipkin, W.I.

J. Virol. 66, 6572-6577, 1992

A/Title: Sequence similarity between Borna disease virus p40 and a duplicated domain w

A/Reference number: A44004; MUID:93021385; PMID:1404604

A/Accession: A44004

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 14-46, 'T', 48-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <MCC>

A/Cross-references: UNIPARC:UPI0000170B06; GB:M99375; NID:G2106598; PIND:AAA73385.1; PI

C/Superfamily: borna disease virus p40

Query Match 99.9%; Score 974; DB 2; Length 370;
Best Local Similarity 99.5%; Pred. No. 8e-86;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:28:28 ; Search time 125.19 Seconds
(without alignments)
663.334 Million cell updates/sec

Title: US-10-627-141-30

Perfect score: 975
Sequence: 1 HTVPSLVPLCLIPGLHAA.....TTIKYLAECMDATLTIPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21: *
1: geneeqp1980s: *
2: geneeqp1990s: *
3: geneeqp2000s: *
4: geneeqp2001s: *
5: geneeqp2002s: *
6: geneeqp2003as: *
7: geneeqp2003bs: *
8: geneeqp2004s: *
9: geneeqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	100.0	189	2 AAW49053	AAW49053 Human Bor
2	974	99.9	370	2 AAR98617	AAR98617 Borna dis
3	969	99.4	189	2 AAW49051	AAW49051 Human Bor
4	960	98.5	189	2 AAW49052	AAW49052 Human Bor
5	328.5	33.7	273	4 AAM42095	AAM42095 Human pol
6	328.5	33.7	273	7 ADE05066	ADE05066 Novel pro
7	328.5	33.7	273	9 ADU40585	ADU40585 Novel hum
8	322.5	33.1	541	8 ADN99838	ADN99838 Novel hum
9	322.5	33.1	541	8 ADN99659	ADN99659 Novel hum
10	315	32.3	208	4 AAM40309	AAM40309 Human pol
11	315	32.3	208	4 AAB92609	AAB92609 Human pro
12	311	31.9	272	9 ADE08030	ADE08030 Novel pro
13	311	31.9	272	9 ADU40400	ADU40400 Novel hum
14	144.5	14.8	85	3 AAB42995	AAB42995 Human ORF
15	94	9.6	90	3 AAB43320	AAB43320 Human ORF
16	89.5	9.2	2225	4 ABB71877	ABB71877 Drosophila
17	87	8.9	270	8 ABB71877	ABB71877 Drosophila
18	87	8.9	396	8 ADX74629	ADX74629 Plant ful
19	85	8.7	82	4 AAM82029	AAM82029 Human hae
20	84.5	8.6	304	4 AEB14344	AEB14344 Plant lip
21	83.5	8.5	1125	8 ADN46700	ADN46700 Thermococ
22	82.5	8.5	988	7 ADM27076	ADM27076 Hyperther
23	81.5	8.4	1190	4 ABB62480	ABB62480 Drosophila
24	79	8.1	782	4 ABB57835	ABB57835 Drosophila

25	78	8.0	620	6 ABU36296	ABU36296 Protein e
26	77.5	7.9	603	8 ADY11308	ADY11308 Plant ful
27	77	7.9	353	6 ABU46953	ABU46953 Protein e
28	77	7.9	420	6 ADA54667	ADA54667 Human pro
29	77	7.9	481	6 ABO27215	ABO27215 Human sig
30	77	7.9	847	6 AAE34446	AAE34446 Human lip
31	77	7.9	847	8 ADS88200	ADS88200 Human pro
32	77	7.9	889	8 ADP55018	ADP55018 Human PRO
33	77	7.9	889	8 ADP97392	ADP97392 Human OSB
34	77	7.9	889	5 ADY16816	ADY16816 PRO polyP
35	76.5	7.8	246	5 ABP45382	ABP45382 Human Bly
36	76.5	7.8	246	7 ADG96209	ADG96209 Single ch
37	76.5	7.8	249	5 ABP45336	ABP45336 Human Bly
38	76.5	7.8	249	7 ADG96163	ADG96163 Single ch
39	76.5	7.8	502	7 ADM05560	ADM05560 Human pro
40	76.5	7.8	1572	4 ABB62868	ABB62868 Drosophila
41	76.5	7.8	1919	5 ABB97422	ABB97422 M. echino
42	76.5	7.8	1919	9 AEB12617	AEB12617 Eneidine
43	76.5	7.8	1919	9 AEC10210	AEC10210 M. echino
44	76.5	7.8	3173	9 ADY16528	ADY16528 E. faecal
45	76	7.8	400	8 ADS23725	ADS23725 Bacterial

ALIGNMENTS

RESULT 1
AAW49053 standard; protein; 189 AA.
ID AAW49053

AAW49053;

27-AUG-2003 (revised)

09-NOV-1998 (first entry)

Human Borna disease virus p40 polypeptide.

BDV; infection; diagnosis; neuropsychiatric disorder; human.

Borna disease virus.

WO9830238-A1.

16-JUL-1998.

07-JAN-1998; 98WO-US000495.

07-JAN-1997; 97US-00779764.

(SCRI) SCRIPPS RES INST.

De La Torre JC;

WPI; 1998-398802/34.

N-PSDB; AAV32853.

New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly:peptide(s), used to develop products for detection.

Claim 12; Fig 11C; 207P; English.

This is the p40 polypeptide of a Borna disease virus (BDV) isolate, designated H3, that was obtained from a psychiatric patient with a mood disorder. Nucleic acids (see AAV32840-55) that encode BDV p24, p16, p56, p40 and L polymerase catalytic domain polypeptides (see AAW49043-53) are provided. These have been obtained from 3 psychiatric patients (isolates H1, H2 and H3) as well as from non-human BDV strain V. Also provided are expression vectors, transformed host cells and antibodies raised against the human BDV polypeptides. Human BDV polypeptides, polynucleotides and antibodies can be used in claimed methods for detecting human BDV or human BDV-like viral infection, particularly in patients with neuropsychiatric disorders. (Updated on 27-AUG-2003 to correct OS field.)

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 ; Search time 113.339 Seconds
(without alignments)
1176.511 Million cell updates/sec

Title: US-10-627-141-30
Perfect score: 975
Sequence: 1 HTVPSLVFLCLIPGHAHA.....TTIKRYLAECMDATITIPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UnIProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	100.0	190	2	065470_BDV
2	974	99.9	370	1	VP40_BDV
3	974	99.9	370	2	010355_BDV
4	974	99.9	370	2	010401_BDV
5	974	99.9	370	2	05GL86_BDV
6	974	99.9	370	2	05GL92_BDV
7	974	99.9	370	2	05GL95_BDV
8	974	99.9	370	2	05GL98_BDV
9	974	99.9	370	2	05GLD1_BDV
10	974	99.9	370	2	08B829_BDV
11	974	99.9	370	2	0910H1_BDV
12	974	99.9	370	2	091U41_BDV
13	974	99.9	370	2	091U48_BDV
14	974	99.9	370	2	0774E9_BDV
15	973	99.8	370	2	010398_BDV
16	970	99.5	370	2	05GL98_BDV
17	969	99.4	190	2	065468_BDV
18	968	99.3	370	2	05GL50_BDV
19	968	99.3	370	2	05GL62_BDV
20	968	99.3	370	2	05GL71_BDV
21	968	99.3	370	2	05GLB3_BDV
22	967	99.2	369	2	09Q9V1_BDV
23	964	98.9	370	2	010392_BDV
24	960	98.5	190	2	065469_BDV
25	908	93.1	176	2	077A29_BDV
26	908	93.1	176	2	077A30_BDV
27	908	93.1	176	2	077A31_BDV
28	908	93.1	176	2	077A32_BDV
29	908	93.1	176	2	077A33_BDV
30	908	93.1	176	2	077A34_BDV
31	908	93.1	176	2	09W8R2_BDV

32	894	91.7	176	2	Q9W17_BDV	Q9W17 borna disea
33	782	80.2	152	2	Q9QCJ2_BDV	Q9QCJ2 borna disea
34	755	77.4	146	2	012852_BDV	012852 borna disea
35	755	77.4	146	2	012853_BDV	012853 borna disea
36	755	77.4	146	2	012855_BDV	012855 borna disea
37	755	77.4	146	2	012856_BDV	012856 borna disea
38	755	77.4	146	2	012857_BDV	012857 borna disea
39	755	77.4	146	2	012858_BDV	012858 borna disea
40	755	77.4	146	2	012859_BDV	012859 borna disea
41	755	77.4	146	2	012860_BDV	012860 borna disea
42	755	77.4	146	2	012861_BDV	012861 borna disea
43	755	77.4	146	2	012862_BDV	012862 borna disea
44	755	77.4	146	2	012863_BDV	012863 borna disea
45	755	77.4	146	2	012864_BDV	012864 borna disea

ALIGNMENTS

RESULT 1	ID	Q65470_BDV	PRELIMINARY;	PRT;	190 AA.
AC	Q65470;				
DT	01-NOV-1996	(TREMblrel. 01, Created)			
DT	01-NOV-1996	(TREMblrel. 01, Last sequence update)			
DT	01-MAR-2004	(TREMblrel. 26, Last annotation update)			
DE	P40	(Fragment)			
OS	Borna disease virus (BDV)				
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae; Bornavirus.				
OX	NCBI_TaxID=12455;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=97233500; PubMed=918344;				
RA	Bode L.; Duerwald R.; Rantam P.A.; Perszt R.; Ludwig H.;				
RT	"First isolates of infectious human Borna disease virus from patients with mood disorders."				
RL	Mol. Psychiatry 1:200-212(1996).				
DR	EMBL; U58596; AB05244.1; -; Genomic RNA.				
DR	HSSP; Q01552; IN93.				
DR	InterPro; IPR009441; BDV_P40.				
DR	PANTHER; PTHR10207; BDV_P40; 1.				
DR	Pfam; PF06407; BDV_P40; 1.				
FT	NOV_TER	1	1		
FT	NOV_TER	190	190		
SQ	SEQUENCE	190 AA; 20900 MW; 6647E7AB4A5C49C CRC64;			
Query Match		100.0%; Score 975; DB 2; Length 190;			
Best Local Similarity		100.0%; Pred. No. 9.1e-86;			
Matches	189; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1	HTVPSLVFLCLIPGHAFAVHGVPRESTLSTPIRGEQTVVTKAFYGEKTTORDLT	60		
DB	1	HTVPSLVFLCLIPGHAFAVHGVPRESTLSTPIRGEQTVVTKAFYGEKTTORDLT	60		
QY	61	ELRISSTFSHCCSLLIGVTVGSSSKIKAGBOIKKFKTMAALNRPDSHGRTATLQMFN	120		
DB	61	ELRISSTFSHCCSLLIGVTVGSSSKIKAGBOIKKFKTMAALNRPDSHGRTATLQMFN	120		
QY	121	PHEAIDINQPMWGSFVLSLLTTDFSPKKEFMDQIKLVASVQMTTYYTIKRYLABCM	180		
DB	121	PHEAIDINQPMWGSFVLSLLTTDFSPKKEFMDQIKLVASVQMTTYYTIKRYLABCM	180		
QY	181	DATLTIPV 189			
DB	181	DATLTIPV 189			
RESULT 2					
VP40_BDV		STANDARD;	PRT;	370 AA.	
AC	Q01552;				
DT	01-JUL-1993	(Rel. 26, Created)			

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:55:45 ; Search time 12.4582 Seconds
(without alignments)
143.427 Million cell updates/sec

Title: US-10-627-141-29

Perfect score: 974
Sequence: 1 HWTPSLVFLCLIPGLHAA.....TTIKYLAECMDATLTPVY 189

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA New:
1: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB pep:*
2: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB pep:*
3: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB pep:*
4: /cgn2_6/prodata/2/pubppa/PC1_NEW_PUB pep:*
5: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB pep:*
6: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB pep:*
7: /cgn2_6/prodata/2/pubppa/US11_NEW_PUB pep:*
8: /cgn2_6/prodata/2/pubppa/US00_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75.5	7.8	246	US-11-054-515-1393	Sequence 1393, App
2	75.5	7.8	249	US-11-054-515-1347	Sequence 1347, App
3	74.5	7.6	1474	US-10-995-561-873	Sequence 873, App
4	70	7.2	4655	US-10-995-561-556	Sequence 556, App
5	69.5	7.1	753	US-10-858-730-225	Sequence 225, App
6	68	7.0	158	US-11-074-176-326	Sequence 326, App
7	68	7.0	172	US-11-074-176-94	Sequence 94, App
8	68	7.0	249	US-11-054-515-1296	Sequence 1296, App
9	68	7.0	251	US-11-054-515-1669	Sequence 1669, App
10	68	7.0	456	US-11-074-176-238	Sequence 238, App
11	67.5	6.9	442	US-10-467-657-1614	Sequence 1614, App
12	66.5	6.8	151	US-10-793-626-1646	Sequence 1646, App
13	66.5	6.8	350	US-11-082-389-280	Sequence 380, App
14	65.5	6.7	356	US-11-052-554A-12	Sequence 12, App
15	65.5	6.7	572	US-10-454-437-68	Sequence 68, App
16	65.5	6.7	584	US-10-454-437-66	Sequence 66, App
17	65	6.7	240	US-10-821-234-1003	Sequence 1003, App
18	65	6.7	300	US-10-793-626-1900	Sequence 1900, App
19	65	6.7	364	US-11-087-177-33	Sequence 33, App
20	65	6.7	374	US-10-517-939-340	Sequence 340, App
21	65	6.7	871	US-10-933-025-3	Sequence 3, App
22	64.5	6.6	391	US-10-613-744-13	Sequence 13, App
23	64.5	6.6	539	US-10-514-250A-28	Sequence 28, App
24	64.5	6.6	539	US-10-514-250A-29	Sequence 29, App
25	64.5	6.6	539	US-10-514-250A-30	Sequence 30, App

26	64.5	6.6	539	US-10-514-250A-31	Sequence 31, App
27	64.5	6.6	539	US-10-514-250A-32	Sequence 32, App
28	64.5	6.6	539	US-10-514-250A-33	Sequence 33, App
29	64.5	6.6	539	US-10-514-250A-34	Sequence 34, App
30	64	6.6	374	US-10-517-939-336	Sequence 336, App
31	64	6.6	854	US-10-511-657-4	Sequence 4, App
32	63	6.5	359	US-10-055-877-265	Sequence 265, App
33	63	6.5	359	US-11-080-091-1	Sequence 1, App
34	63	6.5	359	US-11-116-939-15	Sequence 15, App
35	63	6.5	359	US-11-087-177-23	Sequence 23, App
36	63	6.5	359	US-11-087-177-25	Sequence 25, App
37	63	6.5	359	US-11-043-542-12	Sequence 12, App
38	63	6.5	359	US-11-087-177-31	Sequence 31, App
39	63	6.5	359	US-11-087-177-27	Sequence 27, App
40	63	6.5	357	US-11-043-542-10	Sequence 10, App
41	63	6.5	372	US-11-043-542-8	Sequence 8, App
42	63	6.5	373	US-11-043-542-14	Sequence 14, App
43	63	6.5	385	US-11-043-542-4	Sequence 4, App
44	63	6.5	385	US-11-043-542-6	Sequence 6, App
45	63	6.5	452	US-10-467-962B-14	Sequence 14, App

ALIGNMENTS

RESULT 1
US-11-054-515-1393
Sequence 1393, Application US/11054515
GENERAL INFORMATION:
Publication No. US2005025532A1
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
FILE REFERENCE: PFS2P3
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1393
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1393

Query Match 7.8%; Score 75.5; DB 7; Length 246;
Best local Similarity 22.5%; Pred. No. 0.88;
Matches 27; Conservative 17; Mismatches 43; Indels 33; Gaps 6;

QY 79 VIGSSKIKAEADQIKKFTTMAAVNRSHGETATLLOFNPHDAIDWT-----NCQPV 133
DB 4 LVQSGAEVKKPQGSVAVKSCVA-----SGEN-----FNSY-AISWROAPGQGPFW 47
QY 134 VGSFVSLITTDPSGSKEMDQIKLVASVAKMTYTTTKE-----YLAECMDATL 184

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:54:39 ; Search time 117.593 Seconds
(without alignments)
671.550 Million cell updates/sec

Title: US-10-627-141-29

Perfect score: 974

Sequence: 1 HTWPSLVFLCLIPGLHAA.....TTIKYLAECMDATLTPV 189

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974	100.0	189	4	US-10-627-141-29
2	960	98.6	189	4	US-10-627-141-30
3	954	97.9	189	4	US-10-627-141-28
4	329.5	33.8	273	5	US-10-128-558-370
5	312	32.0	272	5	US-10-128-558-185
6	96.5	9.9	940	4	US-10-437-963-197289
7	96.5	9.9	1350	4	US-10-437-963-125423
8	92.5	9.5	1186	4	US-10-437-963-197319
9	90	9.2	238	4	US-10-291-190-25
10	85	8.7	82	3	US-09-796-692-3393
11	85	8.7	82	4	US-10-040-862-6393
12	85	8.7	82	4	US-10-057-475B-2393
13	85	8.7	82	4	US-10-154-884B-2393
14	85	8.7	82	4	US-10-764-324-2393
15	84.5	8.7	2225	6	US-11-097-143-4243
16	83	8.5	129	4	US-10-424-599-23726
17	82.5	8.5	2323	4	US-10-437-963-197361
18	82	8.4	1159	4	US-10-437-963-197387
19	81.5	8.4	304	6	US-11-021-619-22
20	81.5	8.4	1959	4	US-10-437-963-154458
21	81.5	8.4	2076	4	US-10-437-963-197291
22	81	8.3	782	6	US-11-097-143-297
23	81	8.3	1346	4	US-10-437-963-189131
24	80.5	8.3	538	4	US-10-282-122A-60329
25	80.5	8.3	870	4	US-10-437-963-154457
26	80.5	8.3	1205	4	US-10-437-963-197324
27	80	8.2	270	4	US-10-425-114-56047

28	80	8.2	396	4	US-10-425-114-43995	Sequence 43995, A
29	80	8.2	585	4	US-10-424-599-237273	Sequence 237273, A
30	79.5	8.2	1919	4	US-10-152-886-13	Sequence 13, Appl
31	79.5	8.2	1919	6	US-11-053-576-13	Sequence 13, Appl
32	79.5	8.2	1919	6	US-11-053-052-13	Sequence 13, Appl
33	78.5	8.1	502	4	US-10-108-260A-4245	Sequence 4245, Ap
34	78.5	8.1	912	5	US-10-732-923-6851	Sequence 6851, Ap
35	78.5	8.1	912	5	US-10-732-923-6852	Sequence 6852, Ap
36	78.5	8.1	914	5	US-10-732-923-6854	Sequence 6854, Ap
37	78.5	8.1	965	4	US-10-437-963-160354	Sequence 160354, A
38	78.5	8.1	1278	4	US-10-437-963-181016	Sequence 181016, A
39	77.5	8.0	937	4	US-10-437-963-197334	Sequence 197334, A
40	77.5	8.0	1572	6	US-11-097-143-15396	Sequence 15396, A
41	77	7.9	335	5	US-10-732-923-13080	Sequence 13080, A
42	77	7.9	353	4	US-10-282-122A-74877	Sequence 74877, A
43	77	7.9	400	4	US-10-369-493-12758	Sequence 12758, A
44	77	7.9	457	4	US-10-282-122A-63026	Sequence 63026, A
45	77	7.9	2179	4	US-10-224-999A-3481	Sequence 3481, Ap

ALIGNMENTS

RESULT 1
US-10-627-141-29
Sequence 29, Application US/10627141
Publication No. US20040162421A1
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSER: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 North Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,141
FILING DATE: 25-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-627-141-29
Query Match 100.0%; Score 974; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 6.7e-101;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 HTWPSLVFLCLIPGLHAAFGVGRSSTPTTRGQTVKTAFFYGEKTTORDLT 60
|||||

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:40:34 ; Search time 32.8167 Seconds
(without alignments)
476.151 Million cell updates/sec

Title: US-10-627-141-29

Perfect score: 974

Sequence: 1 HTVTPSLVFLCLIPGHAFA.....TTIKYLAECMDATITIPV 189

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/PTCUB_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfillset.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974	100.0	189	2	US-08-779-764A-29 Sequence 29, Appl
2	974	100.0	189	2	US-09-563-456-29 Sequence 29, Appl
3	960	98.6	189	2	US-08-779-764A-30 Sequence 30, Appl
4	960	98.6	189	2	US-09-563-456-30 Sequence 30, Appl
5	959	98.5	370	2	US-08-369-822C-2 Sequence 2, Appl
6	959	98.5	370	2	US-08-582-776C-2 Sequence 2, Appl
7	959	98.5	370	2	US-08-434-831B-2 Sequence 2, Appl
8	954	97.9	189	2	US-08-779-764A-28 Sequence 28, Appl
9	954	97.9	189	2	US-09-563-456-28 Sequence 28, Appl
10	80.5	8.3	568	2	US-09-489-039A-13755 Sequence 13755, A
11	79.5	8.2	1919	2	US-10-152-886-13 Sequence 13, Appl
12	77.5	8.0	409	2	US-09-270-767-42348 Sequence 42348, A
13	77.5	7.9	488	2	US-09-540-236-1027 Sequence 3027, Ap
14	76	7.8	534	1	US-08-577-184-2 Sequence 2, Appl
15	75.5	7.8	346	2	US-09-724-224-6 Sequence 6, Appl
16	75.5	7.8	346	2	US-10-093-317-6 Sequence 6, Appl
17	75.5	7.8	370	2	US-09-724-224-2 Sequence 2, Appl
18	75.5	7.8	370	2	US-10-093-317-2 Sequence 2, Appl
19	75.5	7.8	487	2	US-09-724-224-8 Sequence 8, Appl
20	75.5	7.8	487	2	US-10-093-317-8 Sequence 8, Appl
21	75.5	7.8	490	2	US-09-949-016-8784 Sequence 8784, Ap
22	75.5	7.8	512	2	US-09-724-224-4 Sequence 4, Appl
23	75.5	7.8	512	2	US-10-093-317-4 Sequence 4, Appl
24	75.5	7.8	665	2	US-09-595-684B-35 Sequence 35, Appl
25	75	7.7	761	2	US-09-328-352-5650 Sequence 5650, Ap
26	74.5	7.6	1474	2	US-09-241-606-2 Sequence 2, Appl
27	74.5	7.6	1474	2	US-09-949-002-287 Sequence 287, App

28	74.5	7.6	1491	2	US-09-949-002-434 Sequence 434, App
29	74	7.6	470	2	US-09-252-991A-25558 Sequence 25558, A
30	73.5	7.5	211	2	US-09-543-681A-6708 Sequence 6708, Ap
31	73	7.5	224	2	US-09-134-000C-3941 Sequence 3941, Ap
32	73	7.5	241	2	US-09-791-540-6 Sequence 6, Appl
33	73	7.5	241	2	US-09-791-578-6 Sequence 6, Appl
34	73	7.5	262	1	US-08-323-445A-4 Sequence 4, Appl
35	73	7.5	262	1	US-08-515-903A-4 Sequence 4, Appl
36	73	7.5	262	4	PCT-US95-12840-4 Sequence 4, Appl
37	73	7.5	264	1	US-08-323-445A-8 Sequence 8, Appl
38	73	7.5	264	1	US-08-515-903A-8 Sequence 8, Appl
39	73	7.5	264	4	PCT-US95-12840-8 Sequence 8, Appl
40	73	7.5	381	1	US-08-687-355A-6 Sequence 6, Appl
41	73	7.5	381	2	US-09-407-367-6 Sequence 6, Appl
42	73	7.5	483	1	US-08-392-338A-19 Sequence 19, Appl
43	73	7.5	483	2	US-09-166-750-19 Sequence 19, Appl
44	73	7.5	483	2	US-09-166-093-19 Sequence 19, Appl
45	73	7.5	483	2	US-09-172-019-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-779-764A-29
Sequence 29, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-764A-29
Query Match 100.0%; Score 974; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.2e-108;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HTVTPSLVFLCLIPGHAFAFHGVPRRESYSTPTTRGQTVKTAEPYGEKTTORDLT 60
DB 1 HTVTPSLVFLCLIPGHAFAFHGVPRRESYSTPTTRGQTVKTAEPYGEKTTORDLT 60
QY 61 ELTISSTFGSCSLTIGVVGSSSKTKAKAEQIKKKPKTMMAAVNPSSHETATLLOMFN 120

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OM protein - protein search, using SW model

Run on: January 17, 2006, 15:33:18 ; Search time 18.2315 Seconds
(without alignments)
997.447 Million cell updates/sec

Title: US-10-627-141-29

Perfect score: 974
Sequence: 1 HTVPSLVPLCLIPGLHAA.....TTIKYLAECMDATLTIPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	959	98.5	370	2	A49528
2	82	8.4	1067	2	D96545
3	80	8.2	448	1	A71659
4	80	8.2	908	2	SS1293
5	79.5	8.2	389	1	SVBJCF
6	78.5	8.1	350	2	AC0813
7	78	8.0	408	2	T32237
8	77	7.9	684	2	A82134
9	77	7.9	1252	1	B42771
10	76	7.8	322	1	S31087
11	76	7.8	340	1	C96655
12	75	7.8	497	2	B82721
13	75.5	7.8	200	2	D90133
14	75.5	7.8	311	2	AH2153
15	75.5	7.8	337	2	A10061
16	75.5	7.8	493	2	C71903
17	75.5	7.8	2180	2	A46182
18	75	7.7	216	2	F83051
19	75	7.7	335	2	AB0963
20	75	7.7	620	2	S73809
21	75	7.7	849	2	S77217
22	75	7.7	2123	2	SS5089
23	74.5	7.6	452	2	ER2387
24	74.5	7.6	592	2	ER5032
25	74.5	7.6	803	2	T00092
26	74.5	7.6	920	2	T10052
27	74.5	7.6	1474	1	MAHU
28	74	7.6	427	2	D83347
29	74	7.6	472	2	B87188

30	74	7.6	507	2	B89792	hypothetical prote
31	74	7.6	678	2	AE0948	probable glycosyl
32	74	7.6	828	2	T12184	probable transcrip
33	74	7.6	857	2	C97707	clpB protein (limp
34	73.5	7.5	224	1	S74541	negative regulator
35	73.5	7.5	383	2	S71191	thiamin biosynthes
36	73.5	7.5	349	2	H86232	hypothetical prote
37	73.5	7.5	662	2	C54078	methy1-accepting c
38	73.5	7.5	872	2	S76197	endopeptidase Clp
39	73.5	7.5	4859	2	S74173	ryanodine receptor
40	73	7.5	164	2	C82629	hypothetical prote
41	73	7.5	233	2	B61222	cytochrome-c oxida
42	73	7.5	315	2	AC2462	two-component resp
43	73	7.5	373	2	A86859	hypothetical prote
44	73	7.5	402	2	AF1929	hypothetical prote
45	73	7.5	1021	2	T42634	connectin/titin -

ALIGNMENTS

RESULT 1

probable structural component p40 - borna disease virus

N:Alternate names: 39K antigen

C:Species: borna disease virus

C>Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text_change 28-Jul-2000

C/Accession: A49528; A37475; S25642; A44004

R/Schneider, P.A.; Brisse, T.; Zimmermann, W.; Ludwig, H.; Lipkin, W.I.

J. Virol. 68, 63-68, 1994

A>Title: Sequence conservation in field and experimental isolates of Borna disease virus

A/Reference number: A49528; MUID:94076462; PMID:8254777

A/Accession: A49528

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 1-370 <SCH>

A/Cross-references: UNIPARC:UPI0000171068; GB:S67502; NID:9456883; PIDN:AA829214.1; PI

A/Note: Sequence extracted from NCBI backbone (NCBIN:141399, NCBI:141401)

R/Pyper, J.M.; Richt, J.A.; Brown, L.; Rott, R.; Narayan, O.; Clements, J.E.

Virol. 195, 229-238, 1993

A>Title: Genomic organization of the structural proteins of borna disease virus reveal.

A/Reference number: A37475; MUID:93303922; PMID:8317098

A/Accession: A37475

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <PYP>

A/Cross-references: UNIPARC:UPI0000170E05; GB:S62821; NID:9386390; PIDN:AA827261.1; PI

A/Note: Sequence extracted from NCBI backbone (NCBIN:134146, NCBI:134147)

R/Binz, T.; Riehle, H.; Yamasaki, J.; Richt, J.A.; Gredemeyer, O.; Rott, R.; Niemann, S.

Submitted to the EMU Data Library, September 1992

A/Description: The 39/39K antigen of borna disease virus.

hypothetical prote

probable glycosyl

probable transcrip

clpB protein (limp

negative regulator

thiamin biosynthes

hypothetical prote

methy1-accepting c

endopeptidase Clp

ryanodine receptor

hypothetical prote

cytochrome-c oxida

two-component resp

hypothetical prote

hypothetical prote

connectin/titin -

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:28:28 ; Search time 125.19 Seconds
(without alignments)
663.334 Million cell updates/sec

Title: US-10-627-141-29

Perfect score: 974
Sequence: 1 HTVPSLVPLCLLPLGLHAA.....TTIKYLAECMDATLTTPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 21:*

1:	Geneseqp19908:*
2:	Geneseqp19908:*
3:	Geneseqp20008:*
4:	Geneseqp20018:*
5:	Geneseqp20028:*
6:	Geneseqp20038:*
7:	Geneseqp20038:*
8:	Geneseqp20048:*
9:	Geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974	100.0	189	2	AAW49052 Human Bor
2	960	98.6	189	2	AAW49053 Human Bor
3	959	98.5	370	2	AAW49051 Human Bor
4	954	97.9	189	2	AAW49051 Human Bor
5	329.5	33.8	273	4	AAW42095 Human pol
6	329.5	33.8	273	7	ADW09066 Human pol
7	329.5	33.8	273	4	ADW09066 Human pol
8	323.5	33.2	541	8	ADW09066 Human pol
9	323.5	33.2	541	8	ADW09066 Human pol
10	316	32.4	208	4	AAW40309 Human pol
11	316	32.4	208	4	AAW40309 Human pol
12	312	32.0	272	7	ADW09066 Human pol
13	312	32.0	272	7	ADW09066 Human pol
14	141.5	14.5	85	3	AAW43320 Human ORF
15	93	9.5	90	3	AAW43320 Human ORF
16	86.5	8.9	988	7	AAW43320 Human ORF
17	85	8.7	82	4	AAW43320 Human ORF
18	84.5	8.7	2225	4	AAW43320 Human ORF
19	82	8.4	1067	5	AAW43320 Human ORF
20	81.5	8.4	1067	5	AAW43320 Human ORF
21	81.5	8.4	1125	8	AAW43320 Human ORF
22	81	8.3	782	4	AAW43320 Human ORF
23	80.5	8.3	538	6	AAW43320 Human ORF
24	80.5	8.3	568	7	AAW43320 Human ORF

25	80	8.2	270	8	ADW493383
26	80	8.2	395	8	ADW493383
27	79.5	8.2	1919	5	ADW493383
28	79.5	8.2	1919	5	ADW493383
29	79.5	8.2	1919	5	ADW493383
30	78.5	8.1	502	7	ADW493383
31	77.5	8.0	468	5	ADW493383
32	77.5	8.0	468	5	ADW493383
33	77.5	8.0	1572	4	ADW493383
34	77	7.9	353	6	ADW493383
35	77	7.9	400	8	ADW493383
36	77	7.9	457	6	ADW493383
37	77	7.9	488	8	ADW493383
38	77	7.9	1254	2	ADW493383
39	77	7.9	1254	2	ADW493383
40	77	7.9	2179	7	ADW493383
41	76.5	7.9	266	2	ADW493383
42	76.5	7.9	1719	4	ADW493383
43	76	7.8	322	3	ADW493383
44	76	7.8	534	2	ADW493383
45	76	7.8	534	2	ADW493383

ALIGNMENTS

RESULT 1
ID AAW49052 standard; protein, 189 AA.
XX AAW49052;
XX AC
XX 27-AUG-2003 (revised)
DT 09-NOV-1998 (first entry)
DT
XX
DE Human Borna disease virus p40 polypeptide.
XX
XX BDV, infection; diagnosis; neuropsychiatric disorder; human.
XX Borna disease virus.
OS
XX W09830238-A1.
XX 16-JUL-1998.
XX
XX 07-JAN-1998; 98WO-US000495.
XX 07-JAN-1997; 97US-00779764.
XX
XX (SCRI) SCRIIPS RES INST.
XX De La Torre JC;
XX WPI, 1998-398802/34.
XX N-PSDB; AAW32852.
XX
XX New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly:peptide(s), used to develop products for detection.
XX Claim 12; Fig 11B; 207P; English.
XX
XX This is the p40 polypeptide of a Borna disease virus (BDV) isolate, designated H2, that was obtained from a psychiatric patient with a mood disorder. Nucleic acids (see AAW32840-55) that encode BDV p24, p16, p56, p40 and L polymerase catalytic domain poly:peptides (see AAW39043-63) are provided. These have been obtained from 3 psychiatric patients (isolates H1, H2 and H3) as well as from non-human BDV strain V. Also provided are expression vectors, transformed host cells and antibodies raised against the human BDV polypeptides. Human BDV polypeptides, polynucleotides and antibodies can be used in claimed methods for detecting human BDV or human BDV-like viral infection, particularly in patients with neuropsychiatric disorders. (Updated on 27-AUG-2003 to correct OS field.)

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 ; Search time 113.339 Seconds
(without alignments)
1176.511 Million cell updates/sec

Title: US-10-627-141-29

Perfect score: 974
Sequence: 1 HTVTPSLVFLCLILPGHAA.....TTIKETLAECMDATLTIPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	974	100.0	190	2	Q65469_BDV
2	960	98.6	190	2	Q65470_BDV
3	959	98.5	370	1	VP40_BDV
4	959	98.5	370	2	O10395_BDV
5	959	98.5	370	2	O10401_BDV
6	959	98.5	370	2	Q5GL86_BDV
7	959	98.5	370	2	Q5GL92_BDV
8	959	98.5	370	2	Q5GL95_BDV
9	959	98.5	370	2	O5GLD1_BDV
10	959	98.5	370	2	O5GLD8_BDV
11	959	98.5	370	2	O8BB29_BDV
12	959	98.5	370	2	Q910H1_BDV
13	959	98.5	370	2	Q910U4_BDV
14	959	98.5	370	2	Q91UJ8_BDV
15	959	98.5	370	2	Q774F9_BDV
16	958	98.4	370	2	O10398_BDV
17	955	98.0	370	2	O5GL98_BDV
18	954	97.9	190	2	Q65468_BDV
19	953	97.8	370	2	Q5GL50_BDV
20	953	97.8	370	2	O5GL62_BDV
21	953	97.8	370	2	O5GL71_BDV
22	953	97.8	370	2	O5GL83_BDV
23	952	97.7	369	2	Q9Q9V1_BDV
24	949	97.4	370	2	O10392_BDV
25	893	91.7	176	2	Q77A29_BDV
26	893	91.7	176	2	Q77A30_BDV
27	893	91.7	176	2	Q77A31_BDV
28	893	91.7	176	2	Q77A32_BDV
29	893	91.7	176	2	Q77A33_BDV
30	893	91.7	176	2	Q77A34_BDV
31	893	91.7	176	2	Q9W8R2_BDV

32	879	90.2	176	2	Q9W117_BDV	Q9W117 borna disea
33	767	78.7	152	2	Q9QCJ2_BDV	Q9QCJ2 borna disea
34	740	76.0	146	2	O12852_BDV	O12852 borna disea
35	740	76.0	146	2	O12853_BDV	O12853 borna disea
36	740	76.0	146	2	O12855_BDV	O12855 borna disea
37	740	76.0	146	2	O12856_BDV	O12856 borna disea
38	740	76.0	146	2	O12857_BDV	O12857 borna disea
39	740	76.0	146	2	O12858_BDV	O12858 borna disea
40	740	76.0	146	2	O12859_BDV	O12859 borna disea
41	740	76.0	146	2	O12860_BDV	O12860 borna disea
42	740	76.0	146	2	O12861_BDV	O12861 borna disea
43	740	76.0	146	2	O12862_BDV	O12862 borna disea
44	740	76.0	146	2	O12863_BDV	O12863 borna disea
45	740	76.0	146	2	O12864_BDV	O12864 borna disea

ALIGNMENTS

RESULT 1	ID	Seq	Score	Length	DB ID	Description
Q65469_BDV	Q65469_BDV	PRELIMINARY;	PRT;	190 AA.		
AC	Q65469;					
DT	01-NOV-1996 (Tremblrel. 01, Created)					
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)					
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)					
DE	P40 (Fragment).					
OS	Borna disease virus (BDV).					
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;					
OC	Bornavirus.					
OX	NCBI_TaxID=12455;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RA	MEDLINE=97233300; PubMed=9118344;					
RX	Bode L., Dietz R., Rantam F.A., Persz R., Ludwig H.;					
RT	"First isolates of infectious human Borna disease virus from patients with mood disorders."					
RL	Mol. Psychiatry 1:200-212 (1996).					
DR	EMBL; U58595; AAB05243.1; --; Genomic_RNA.					
DR	HSSP; Q01552; IN93.					
DR	InterPro; IPR009441; BDV_P40.					
DR	PANTHER; PTR10207; BDV_P40; 1.					
FT	Pfam: PF06407; BDV_P40; 1.					
FT	NON_TER					
FT	NON_TER					
SQ	SEQUENCE	190 AA; 20959 MM; 0B6CCCC12EA62683 CRC64;				
Query Match		100.0%; Score 974; DB 2; Length 190;				
Best Local Similarity		100.0%; Pred. No. 2, 9e-84;				
Matches	189;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	HTVTPSLVFLCLILPGHAAFHVGVPRESYSTPTTRGQTVVKTNAEPFGKTDQDLT	60			
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QY	61	ELHISSTFSCGSLIGVIGSSSKIKAEQIKKPKTMAAVNPSHGETATLQMFN	120			
DB	61	ELHISSTFSCGSLIGVIGSSSKIKAEQIKKPKTMAAVNPSHGETATLQMFN	120			
QY	121	PHEAIDWINGQPMWGSFVLSLTTFDESPEKEFMDQIKLVASYAQMNTTYTIKEYLABCM	180			
DB	121	PHEAIDWINGQPMWGSFVLSLTTFDESPEKEFMDQIKLVASYAQMNTTYTIKEYLABCM	180			
QY	181	DATLTIPV 189				
DB	181	DATLTIPV 189				
RESULT 2						
ID	Q65470_BDV	PRELIMINARY;	PRT;	190 AA.		
ID	Q65470;					
DT	01-NOV-1996 (Tremblrel. 01, Created)					

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:54:39 ; Search time 117.593 Seconds
(without alignments)
671.550 Million cell updates/sec

Title: US-10-627-141-28

Perfect score: 978
Sequence: 1 HTWPSLWFLCLIPGLHAA.....TTIKYLAECMDATLTIPV 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main: *
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	969	99.1	189	4 US-10-627-141-30	Sequence 30, App1
3	954	97.5	189	4 US-10-627-141-29	Sequence 29, App1
4	327.5	53.5	273	5 US-10-128-558-370	Sequence 370, App
5	310	31.7	272	5 US-10-128-558-185	Sequence 185, App1
6	89	9.1	238	4 US-10-291-190-25	Sequence 25, App1
7	88.5	9.0	1350	4 US-10-437-963-197289	Sequence 197289, App
8	88.5	9.0	1350	4 US-10-437-963-125423	Sequence 125423, App
9	88.5	9.0	2225	6 US-11-097-143-42423	Sequence 42423, App
10	86	8.8	82	3 US-09-796-692-2393	Sequence 2393, App
11	86	8.8	82	4 US-10-040-862-2393	Sequence 2393, App
12	86	8.8	82	4 US-10-057-475B-2393	Sequence 2393, App
13	86	8.8	82	4 US-10-154-884B-2393	Sequence 2393, App
14	86	8.8	82	4 US-10-764-324-2393	Sequence 2393, App
15	85	8.7	129	4 US-10-424-599-237276	Sequence 237276, App
16	84.5	8.6	1186	4 US-10-437-963-197319	Sequence 197319, App
17	83.5	8.5	304	6 US-11-021-619-42	Sequence 42, App1
18	82	8.4	270	4 US-10-425-114-56047	Sequence 56047, App
19	82	8.4	396	4 US-10-425-114-43995	Sequence 43995, App
20	82	8.4	439	4 US-10-282-122A-50928	Sequence 50928, App
21	82	8.4	585	4 US-10-424-599-237273	Sequence 237273, App
22	80.5	8.2	1190	4 US-11-097-143-14232	Sequence 14232, App
23	79.5	8.1	1919	4 US-10-152-886-13	Sequence 13, App1
24	79.5	8.1	1919	6 US-11-053-576-13	Sequence 13, App1
25	79.5	8.1	1919	6 US-11-053-052-13	Sequence 13, App1
26	79	8.1	782	6 US-11-097-143-297	Sequence 297, App
27	79	8.1	1159	4 US-10-437-963-129387	Sequence 129387, App

28	77.5	7.9	1959	4 US-10-437-963-154458	Sequence 154458, App
29	77.5	7.9	2076	4 US-10-437-963-197291	Sequence 197291, App
30	77	7.9	420	4 US-10-094-749-2235	Sequence 2235, App
31	77	7.9	481	3 US-09-955-999-104	Sequence 104, App
32	77	7.9	847	4 US-10-478-245-7	Sequence 245, App1
33	77	7.9	1346	4 US-10-437-963-189131	Sequence 189131, App
34	76.5	7.8	246	3 US-09-880-768-1393	Sequence 1393, App
35	76.5	7.8	246	4 US-10-293-418-1393	Sequence 1393, App
36	76.5	7.8	249	3 US-09-880-748-1347	Sequence 1347, App
37	76.5	7.8	249	4 US-10-293-418-1347	Sequence 1347, App
38	76.5	7.8	447	4 US-10-282-122A-48992	Sequence 48992, App
39	76.5	7.8	870	4 US-10-437-963-154457	Sequence 154457, App
40	76.5	7.8	1205	4 US-10-437-963-197324	Sequence 197324, App
41	76.5	7.8	1563	4 US-10-437-963-190562	Sequence 190562, App
42	76	7.8	353	4 US-10-282-122A-74877	Sequence 74877, App
43	76	7.8	400	4 US-10-369-493-12758	Sequence 12758, App
44	76	7.8	527	4 US-10-437-963-203871	Sequence 203871, App
45	75.5	7.7	400	4 US-10-335-977-5588	Sequence 5588, App

ALIGNMENTS

RESULT 1
US-10-627-141-28
Sequence 28, Application US/10627141
Publication No. US20040162421A1
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 North Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,141
CLASSIFICATION: 435
FILING DATE: 25-Jul-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
MOLECULAR TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-627-141-28
Query Match 100.0%; Score 978; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 7.4e-103;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 HTWPSLWFLCLIPGLHAAFYHGCVRSYSTPTVTRGQVTKTKFKYGEKTTQDRT 60
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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:40:34 ; Search time 32.8167 Seconds
(without alignments)
476.151 Million cell updates/sec

Title: US-10-627-141-28

Perfect score: 978
Sequence: 1 HTTPELVFLCLIPGILHA.....TIKEYLABCMATLIPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/1/aa/6 COMB.pep.*
3: /cgn2_6/prodata/1/aa/H COMB.pep.*
4: /cgn2_6/prodata/1/aa/PC/US COMB.pep.*
5: /cgn2_6/prodata/1/aa/RB COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	100.0	189	2	US-08-779-764A-28
2	978	100.0	189	2	US-09-563-456-28
3	970	99.2	370	2	US-08-369-822C-2
4	970	99.2	370	2	US-08-582-776C-2
5	970	99.2	370	2	US-08-434-831B-2
6	969	99.1	189	2	US-08-779-764A-30
7	969	99.1	189	2	US-09-563-456-30
8	954	97.5	189	2	US-08-779-764A-29
9	954	97.5	189	2	US-09-563-456-29
10	79.5	8.1	1919	2	US-10-152-886-13
11	76	7.8	534	1	US-08-577-184-2
12	75	7.7	761	2	US-09-328-352-5650
13	74.5	7.6	519	2	US-09-134-000C-4482
14	74	7.6	404	2	US-08-459-953A-7
15	74	7.6	404	2	US-09-393-212-7
16	74	7.6	978	2	US-09-949-016-9804
17	73.5	7.5	409	2	US-09-270-767-42348
18	73	7.5	797	2	US-09-949-016-9859
19	73	7.5	814	2	US-09-198-452A-636
20	72.5	7.4	393	2	US-09-438-185A-596
21	72.5	7.4	393	2	US-08-459-953A-2
22	72.5	7.4	393	2	US-09-393-212-2
23	72.5	7.4	859	2	US-09-302-540-14220
24	72.5	7.4	859	2	US-09-342-648-9
25	72	7.4	367	2	US-09-025-580-24
26	72	7.4	367	2	US-09-642-749-24
27	72	7.4	470	2	US-09-252-991A-25558

28	71.5	7.3	211	2	US-09-543-681A-6708	Sequence 6708, Ap
29	71.5	7.3	1474	2	US-09-241-606-2	Sequence 2, Appl
30	71.5	7.3	1474	2	US-09-949-002-287	Sequence 287, App
31	71.5	7.3	1491	2	US-09-949-002-434	Sequence 434, App
32	71.5	7.3	1721	2	US-10-042-665A-6	Sequence 6, Appl
33	71	7.3	367	2	US-09-457-040B-1	Sequence 1, Appl
34	71	7.3	367	2	US-09-457-040B-33	Sequence 33, Appl
35	71	7.3	367	2	US-09-538-092-1203	Sequence 1203, Ap
36	71	7.3	488	2	US-09-540-236-3027	Sequence 3027, Ap
37	70.5	7.2	362	2	US-09-270-767-41652	Sequence 41652, A
38	70.5	7.2	427	2	US-09-489-039A-12852	Sequence 12852, A
39	70.5	7.2	440	2	US-09-591-095-27	Sequence 27, Appl
40	70.5	7.2	456	2	US-09-949-016-9294	Sequence 9294, Ap
41	70.5	7.2	568	2	US-09-489-039A-13755	Sequence 13755, A
42	69.5	7.1	455	2	US-09-328-352-4555	Sequence 4555, Ap
43	69.5	7.1	919	2	US-09-919-039-222	Sequence 222, App
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ALIGNMENTS

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RESULT 1
US-08-779-764A-28
; Sequence 28, Application US/08779764A
; Patent No. 6057094
; GENERAL INFORMATION:
; APPLICANT: de la Torre, Juan C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
; TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSER: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10550 NO. 6057094th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: United States
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,764A
; FILING DATE: 16-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 465.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-779-764A-28

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Best local Similarity 100.0%; Pred. No. 4.6e-111;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 HTTPELVFLCLIPGILHAFFVGVPRSYSTPTVREBQIVVKTAKYGEKTTORDLT 60
QY 61 EIEISSIFHCSSILIGIVIGSSSKTKAGAEQIKKFKTMALNPSHGETTLQMFN 120
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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:33:18 ; Search time 18.2315 Seconds
(without alignments)
997.447 Million cell updates/sec

Title: US-10-627-141-28

Perfect score: 978

Sequence: 1 HVTPLSLVFLCLIPGLHAA.....TTIKXYLABGMDATLTPV 189

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Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR 80: *
2: PIR: *
3: PIR: *
4: PIR: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	970	99.2	370	2 A49528	probable structural
2	85	8.7	448	1 A71659	DNA repair protein
3	81.5	8.3	311	2 AH2153	hypothetical prote
4	81	8.3	388	2 T36766	probable two-compo
5	81	8.3	1224	2 T19749	hypothetical prote
6	80.5	8.2	200	2 C41873	heat shock protein
7	80.5	8.2	200	2 A97058	molecular chaperon
8	77.5	7.9	332	2 T34758	oligopeptide trans
9	77.5	7.9	675	2 S16625	penicillin-binding
10	77	7.9	408	2 T32337	hypothetical prote
11	77	7.9	666	2 S54401	penicillin-binding
12	77	7.9	1021	2 T42634	connectin/citin
13	76.5	7.8	180	1 FXAVEP	flavodoxin - Azoto
14	76.5	7.8	303	2 AB1937	hypothetical prote
15	76.5	7.8	350	2 AC0813	ethanolamine oporo
16	76.5	7.8	592	2 E75032	carbon starvation
17	76	7.8	1252	2 B42771	reticulocyte-bind
18	75.5	7.7	337	2 A10061	hypothetical prote
19	75.5	7.7	389	1 SYPCF	naringenin-chalcon
20	75.5	7.7	463	1 C71903	D-alanyl-D-alanine
21	75.5	7.7	1303	1 S27396	phytochrome / prot
22	75	7.7	620	2 S73809	DNA primase - Myco
23	75	7.7	792	2 G86564	phenylalanyl tRNA
24	75	7.7	849	2 S77217	phosphorylase (EC
25	75	7.7	2133	2 S55089	probable acetyl-Co
26	74	7.6	388	2 B61222	cytochrome-c oxida
27	74	7.6	388	2 F75162	tryptophan synthas
28	73.5	7.5	352	2 A69743	ATP-binding Msp-1i
29	73.5	7.5	383	2 H86232	hypothetical prote

30	73.5	7.5	457	2 G82187	biopolymer transpo
31	73.5	7.5	920	2 T10052	aminopeptidase (EC
32	73	7.5	792	2 H72058	phenylalanine-cRNA
33	73	7.5	792	2 D81608	phenylalanine-cRNA
34	73	7.5	908	2 S51293	probable membrane
35	73	7.5	1333	2 S65812	RNA-directed DNA p
36	72.5	7.4	248	2 S33756	granzyme-like prot
37	72.5	7.4	37	2 C72276	phosphate ABC tran
38	72.5	7.4	329	2 H71192	hypothetical prote
39	72.5	7.4	885	2 I38968	100 kDa coactivato
40	72	7.4	351	2 T29369	probable lacI-fami
41	72	7.4	427	2 D83347	hypothetical prote
42	72	7.4	433	2 A81723	probable aminotran
43	71.5	7.3	300	2 A81723	ABC transporter (A
44	71.5	7.3	433	2 S05654	ND3 intiron protein
45	71.5	7.3	662	2 C54078	methyl-accepting c

ALIGNMENTS

RESULT 1

A49528
probable structural component p40 - borna disease virus

N/Alternate names: 39K antigen

C/Species: borna disease virus

C/Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000

C/Accession: A49528; A37475; S25642; A44004

J./Schneider, P.A.; Brisse, T.; Zimmermann, W.; Ludwig, H.; Lipkin, W.I.

J. Virol. 68, 63-68, 1994

A./Title: Sequence conservation in field and experimental isolates of Borna disease viru

A./Reference number: A49528; PMID:94076462; PMID:8254777

A./Accession: A49528

A./Status: preliminary

A./Molecule type: genomic RNA

A./Residues: 1-370 <8CH>

A./Cross-references: UNIPARC:UPI000017106E; GB:867502; NID:9456883; PIDN:AMB29214.1; PII

A./Experimental source: WT-1, Halle B1/91, horse brain, field isolate

A./Note: sequence extracted from NCBI backbone (NCBIN:134146, NCBIPI:134147)

R./Pyper, J.M.; Richt, J.A.; Brown, L.; Rott, R.; Narayan, O.; Clements, J.E.

Virol. 195, 229-238, 1993

A./Title: Genomic organization of the structural proteins of borna disease virus reveal

A./Reference number: A37475; PMID:93303922; PMID:8317098

A./Accession: A37475

A./Molecule type: mRNA

A./Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <PYP>

A./Cross-references: UNIPARC:UPI0000170805; GB:862821; NID:9386390; PIDN:AMB27261.1; PII

A./Note: sequence extracted from NCBI backbone (NCBIN:134146, NCBIPI:134147)

R./Binz, T.; Riehle, H.; Yamaoka, J.; Richt, J.A.; Grebenstein, O.; Rott, R.; Niemann,

submitted to the EMBL Data Library, September 1992

A./Description: The 39/39k antigen of borna disease virus.

A./Reference number: S25642

A./Accession: S25642

A./Status: preliminary

A./Molecule type: mRNA

A./Residues: 14-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <BIN>

A./Cross-references: UNIPARC:UPI0000170805; EMBL:X68392; NID:958687; PIDN:CAA48458.1; PII

R./McClure, M.A.; Thibault, K.J.; Hatahara, C.G.; Lipkin, W.I.

J. Virol. 66, 6572-6577, 1992

A./Title: Sequence similarity between Borna disease virus p40 and a duplicated domain wi

A./Reference number: A44004; PMID:93021385; PMID:1404604

A./Accession: A44004

A./Status: preliminary

A./Molecule type: genomic RNA

A./Residues: 14-66, 'T', 48-55, 'N', 57-356, 'I', 358-361, 'R', 363-370 <MCC>

A./Cross-references: UNIPARC:UPI0000170806; GB:M93975; NID:9210698; PIDN:AAA73385.1; PII

C./Superfamily: borna disease virus p40

Query Match 99.2%; Score 970; DB 2; Length 370;

Best Local Similarity 99.5%; Pred. No. 1.2e-84;

Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:48:14 ; Search time 22.1817 Seconds
(without alignments)
348.754 Million cell updates/sec

Title: US-10-627-141-28

Perfect score: 978
Sequence: 1 HTVPSLVFLCLIPGLHAA.....TTIKYLAECMDATITIPV 189

Scoring table:

BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 150911 seqs, 40930936 residues

Total number of hits satisfying chosen parameters: 150911

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents AA New:*
1: /cgn2_6/ptodata/2/paa/PCF NEW COMB pep:*
2: /cgn2_6/ptodata/2/paa/US06 NEW COMB pep:*
3: /cgn2_6/ptodata/2/paa/US07 NEW COMB pep:*
4: /cgn2_6/ptodata/2/paa/US08 NEW COMB pep:*
5: /cgn2_6/ptodata/2/paa/US09 NEW COMB pep:*
6: /cgn2_6/ptodata/2/paa/US10 NEW COMB pep:*
7: /cgn2_6/ptodata/2/paa/US11 NEW COMB pep:*
8: /cgn2_6/ptodata/2/paa/US60 NEW COMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77.5	7.9	1574	US-11-268-554-114	Sequence 114, App
2	77	7.9	847	US-60-742-219-298	Sequence 298, App
3	77	7.9	889	US-60-742-219-300	Sequence 300, App
4	76.5	7.8	246	US-11-266-444-1393	Sequence 1393, App
5	76.5	7.8	246	US-60-735-988-1393	Sequence 1393, App
6	76.5	7.8	249	US-11-266-444-1347	Sequence 1347, App
7	76.5	7.8	249	US-60-735-988-1347	Sequence 1347, App
8	74	7.6	251	US-11-266-444-1669	Sequence 1669, App
9	74	7.6	251	US-60-735-988-1669	Sequence 1669, App
10	74	7.6	1033	US-10-276-817B-14850	Sequence 14850, A
11	74	7.6	1428	US-10-299-791-22	Sequence 22, App1
12	73.5	7.5	3173	US-10-558-119-223	Sequence 223, App
13	73	7.5	472	US-10-276-817B-13919	Sequence 13919, A
14	73	7.5	908	US-60-752-355-12907	Sequence 12907, A
15	72.5	7.4	633	US-60-741-048-47	Sequence 47, App1
16	72.5	7.4	910	US-60-741-048-46	Sequence 46, App1
17	71.5	7.3	485	US-11-311-940-1123	Sequence 1123, App
18	71.5	7.3	506	US-11-311-940-4063	Sequence 4063, App
19	71.5	7.3	1474	US-60-741-051-104	Sequence 104, App
20	71.5	7.3	1474	US-60-741-051-105	Sequence 105, App1
21	71	7.3	367	US-11-303-901-10	Sequence 10, App
22	70.5	7.2	375	US-11-311-940-414	Sequence 414, App
23	70.5	7.2	753	US-60-752-355-3310	Sequence 3310, App
24	70	7.2	475	US-60-752-355-27866	Sequence 27866, A
25	69.5	7.1	396	US-11-311-940-3786	Sequence 3786, App

26	69.5	7.1	733	US-11-311-940-6017	Sequence 6017, App
27	69.5	7.1	753	US-60-752-355-32717	Sequence 32717, A
28	69.5	7.1	875	US-11-289-102-364	Sequence 364, App
29	69	7.1	315	US-60-752-355-30760	Sequence 30760, A
30	69	7.1	315	US-60-752-355-46410	Sequence 46410, A
31	69	7.1	510	US-10-558-119-447	Sequence 447, App
32	68.5	7.0	338	US-60-752-355-32869	Sequence 32869, A
33	68.5	7.0	358	US-60-752-355-26785	Sequence 26785, A
34	68.5	7.0	533	US-60-752-355-21538	Sequence 21538, A
35	68.5	7.0	613	US-60-752-355-35353	Sequence 35353, A
36	68.5	7.0	629	US-10-868-184C-4170	Sequence 4170, App
37	68.5	7.0	634	US-11-311-940-3999	Sequence 3999, App
38	68.5	7.0	753	US-60-752-355-7910	Sequence 7910, App
39	68.5	7.0	753	US-60-752-355-30529	Sequence 30529, A
40	68.5	7.0	753	US-60-752-355-35623	Sequence 35623, A
41	68.5	7.0	1033	US-10-501-841-15	Sequence 15, App1
42	68.5	7.0	3343	US-11-122-396-7	Sequence 7, App1
43	68	7.0	537	US-11-246-765A-72	Sequence 72, App1
44	68	7.0	582	US-60-752-355-18475	Sequence 18475, A
45	67.5	6.9	249	US-11-266-444-1296	Sequence 1296, App

ALIGNMENTS

```

RESULT 1
US-11-268-554-114
; Sequence 114, Application US/11268554
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno et al.
; TITLE OF INVENTION: PANCREATIC CANCER TARGETS AND USES
; FILE REFERENCE: C0001557
; CURRENT APPLICATION NUMBER: US/11/268,554
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 1004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 1574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-268-554-114

Query Match      7.9%; Score 77.5; DB 7; Length 1574;
Best Local Similarity 26.6%; Pred. No. 5.8;
Matches 38; Conservative 14; Mismatches 74; Indels 17; Gaps 5;

Cy 15 PGLAAAFVHGCVPRRESVISTPTVTRGEOIV-KTAKFYGKRTQORDTLRLSISFSSHC 73
Db 1162 PYAHICPLHNSKTTETIHSITNPWTQITIFDEVEIYGEPTVLQNPVKVIMELFDN--- 1218
Cy 74 LLIIGVIGSSSKI---KAGAEQIKRFRKTMALNRPESHGETATLLQFNPHBAIDWING 130
Db 1219 ---DQVVGQANKILHQLGAPERLALHILRTGLVPEHVTITLHSTFGPN--ISQKL 1273
Cy 131 QPWGSGFVLPLLTITDPSPEKEF 153
Db 1274 QMWVDVPPKSP-----GPPGPPF 1291

RESULT 2
US-60-742-219-298
; Sequence 298, Application US/60742219
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John Verner
; APPLICANT: Bradley, Walter Edward
; APPLICANT: Paquin, Bruno
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Little, Randall David
; APPLICANT: Keith, Tim

```

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:28:28 ; Search time 125.19 Seconds
(without alignments)
663.334 Million cell updates/sec

Title: US-10-627-141-28

Perfect score: 978
Sequence: 1 HVTGPSLVFPCLLIPGLHAA.....TTIKYLAECMDATLITPVV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	100.0	189	2	AAW49051 Human Bor
2	970	99.2	370	2	AAR98617 Borna dis
3	969	99.1	189	2	AAW49053 Human Bor
4	954	97.5	189	2	AAW49052 Human Bor
5	327.5	33.5	273	4	AAW42095 Human pol
6	327.5	33.5	273	7	ADBO9066 Novel pro
7	327.5	33.5	273	9	ADU40585 Novel hum
8	321.5	32.9	541	8	ADN99838 Novel hum
9	321.5	32.1	541	8	ADN99838 Novel hum
10	314	32.1	208	4	AAW40309 Human pol
11	314	32.1	208	4	AAW40309 Human pol
12	310	31.7	272	7	ADBO9030 Novel pro
13	310	31.7	272	7	ADU40400 Novel hum
14	144.5	14.8	85	3	AAW42995 Human ORF
15	95	9.7	90	3	AAW43320 Human ORF
16	88.5	9.0	2225	4	ABW71877 Drosophila
17	86.5	8.8	988	7	ADW27076 Hyperther
18	86	8.8	82	4	AAW42029 Human hae
19	83.5	8.5	304	9	ABW14344 Plant lip
20	82	8.4	270	8	ADW49383 Plant ful
21	82	8.4	439	6	ABW74629 Plant ful
22	82	8.4	439	6	ABW74629 Plant ful
23	81	8.3	4984	6	ABW70133 Photocorb
24	80.5	8.2	1125	8	ADW46700 Thermoco

25	80.5	8.2	1190	4	ABB62480 Drosophila
26	79.5	8.1	1919	5	ABG97422 M. echino
27	79.5	8.1	1919	5	ABW12617 Eneidiyne
28	79.5	8.1	1919	9	ABW10210 M. echino
29	79	8.1	782	4	ABW57835 Drosophila
30	77	7.9	420	6	ADW45667 Human pro
31	77	7.9	481	6	ABO27215 Human sig
32	77	7.9	847	6	AAW44446 Human lip
33	77	7.9	847	8	ADW88200 Human pro
34	77	7.9	889	8	ADW55018 Human PRO
35	77	7.9	889	8	ADW97392 Human OSB
36	77	7.9	889	9	ADW16816 PRO poly
37	76.5	7.8	246	5	ABW45382 Human Bly
38	76.5	7.8	246	7	ADW96209 Single ch
39	76.5	7.8	249	5	ABW45336 Human Bly
40	76.5	7.8	249	7	ADW96163 Single ch
41	76.5	7.8	447	6	ABW21068 Protein e
42	76.5	7.8	813	6	ABW70986 Human adi
43	76	7.8	353	6	ABW46953 Protein e
44	76	7.8	400	8	ADW23725 Bacterial
45	76	7.8	534	2	AAW99502 Nitrilase

ALIGNMENTS

RESULT 1
AAW49051 standard; protein; 189 AA.

XX	AAW49051;	
AC	AAW49051;	
XX	27-AUG-2003 (revised)	
DT	09-NOV-1998 (first entry)	
XX		
DE	Human Borna disease virus p40 polypeptide.	
XX		
KM	BDV; infection; diagnosis; neuropsychiatric disorder; human.	
XX		
OS	Borna disease virus.	
XX		
PN	MO9830238-A1.	
XX		
PD	16-JUL-1998.	
XX		
PP	07-JAN-1998; 98WO-US000495.	
XX		
PR	07-JAN-1997; 97US-00779764.	
XX		
PA	(SCRI) SCRIIPS RES INST.	
XX		
PI	De La Torre JC;	
XX		
DR	WPI: 1998-398802/34.	
XX		
PT	N-PSDB; AAW32851.	
PT	New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly:peptide(s), used to develop products for detection.	
XX		
PS	Claim 12; Fig 11A; 207PP; English.	
XX		
CC	This is the p40 polypeptide of a Borna disease virus (BDV) isolate, designated H1, that was obtained from a psychiatric patient with a mood disorder. Nucleic acids (see AAW32840-55) that encode BDV p24, p16, p56, p40 and L polymerase catalytic domain polypeptides (see AAW49043-63) are provided. These have been obtained from 3 psychiatric patients (isolates H1, H2 and H3) as well as from non-human BDV strain V. Also provided are expression vectors, transformed host cells and antibodies raised against the human BDV polypeptides. Human BDV polypeptides, polynucleotides and antibodies can be used in claimed methods for detecting human BDV or human BDV-like viral infection, particularly in patients with neuropsychiatric disorders. (Updated on 27-AUG-2003 to correct OS field.)	

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OM protein - protein search, using sw model

Run on: January 17, 2006, 15:30:13 ; Search time 113.339 Seconds
(without alignments)
1176.511 Million cell updates/sec

Title: US-10-627-141-28

Perfect score: 978
Sequence: 1 HVTPLVFLVCLLIPGLHAA.....TTIKYLAECMDATLTTPV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	100.0	190	2	Q65468_BDV
2	970	99.2	370	1	VP40_BDV
3	970	99.2	370	2	O10395_BDV
4	970	99.2	370	2	O10401_BDV
5	970	99.2	370	2	O5GL86_BDV
6	970	99.2	370	2	O5GL92_BDV
7	970	99.2	370	2	O5GL95_BDV
8	970	99.2	370	2	O5GL98_BDV
9	970	99.2	370	2	O5GLD1_BDV
10	970	99.2	370	2	O8B829_BDV
11	970	99.2	370	2	O910H1_BDV
12	970	99.2	370	2	O91UL4_BDV
13	970	99.2	370	2	O91UL8_BDV
14	970	99.2	370	2	O774E9_BDV
15	969	99.1	190	2	O65470_BDV
16	969	99.1	370	2	O10398_BDV
17	966	98.8	370	2	O5GL98_BDV
18	964	98.6	370	2	O5GL50_BDV
19	964	98.6	370	2	O5GL62_BDV
20	964	98.6	370	2	O5GL71_BDV
21	964	98.6	370	2	O5GLB3_BDV
22	963	98.5	369	2	O9QSV1_BDV
23	960	98.2	370	2	O10392_BDV
24	954	97.5	190	2	O65469_BDV
25	954	97.5	176	2	O77A29_BDV
26	954	97.4	176	2	O77A30_BDV
27	954	97.4	176	2	O77A31_BDV
28	954	97.4	176	2	O77A32_BDV
29	954	97.4	176	2	O77A33_BDV
30	954	97.4	176	2	O77A34_BDV
31	904	92.4	176	2	O9WB82_BDV

32	890	91.0	176	2	O9WN17_BDV	O9WN17	bor	disea
33	778	79.6	152	2	O9QC12_BDV	O9QC12	bor	disea
34	751	76.8	146	2	O12852_BDV	O12852	bor	disea
35	751	76.8	146	2	O12853_BDV	O12853	bor	disea
36	751	76.8	146	2	O12855_BDV	O12855	bor	disea
37	751	76.8	146	2	O12856_BDV	O12856	bor	disea
38	751	76.8	146	2	O12857_BDV	O12857	bor	disea
39	751	76.8	146	2	O12858_BDV	O12858	bor	disea
40	751	76.8	146	2	O12859_BDV	O12859	bor	disea
41	751	76.8	146	2	O12860_BDV	O12860	bor	disea
42	751	76.8	146	2	O12861_BDV	O12861	bor	disea
43	751	76.8	146	2	O12862_BDV	O12862	bor	disea
44	751	76.8	146	2	O12863_BDV	O12863	bor	disea
45	751	76.8	146	2	O12864_BDV	O12864	bor	disea

ALIGNMENTS

RESULT 1	Q65468_BDV	PRELIMINARY;	PRT;	190 AA.
ID	Q65468;			
AC	Q65468;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	P40 (Fragment).			
OS	Borna disease virus (BDV).			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;			
OC	Bornavirus.			
OX	NCBI_TaxID=12455;			
RN	[1]			
RP	NCLEBOTIDE SEQUENCE.			
RX	MEDLINE=97233300; PubMed=9118344;			
RA	Bode L., Duerwald R., Rantam F.A., Ferszt R., Ludwig H.;			
RT	"First isolates of infectious human Borna disease virus from patients with mood disorders."			
RL	Mol. Psychiatry 1:200-212 (1996).			
DR	EMBL; U58594; AAB05242.1; -; Genomic_RNA.			
DR	HSSP; 001552; IN93.			
DR	InterPro; IPR009441; BDV_P40.			
DR	PANTHER; PTHR10207; BDV_P40; 1.			
DR	Pfam; PF06407; BDV_P40; 1.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE	190 AA; 20896 MW; 75FCA881370B9C CRC64;		
Query Match	100.0%; Score 978; DB 2; Length 190;			
Best Local Similarity	100.0%; Pred. No. 1.1e-86;			
Matches 189; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1	HVTPLVFLVCLLIPGLHAAFYHGVGRRESYSTPTVRGQVTVAKKFGKTTORDLT	60	
DB	1	HVTPLVFLVCLLIPGLHAAFYHGVGRRESYSTPTVRGQVTVAKKFGKTTORDLT	60	
QY	61	ELKISIFSHCCSLILGIVIGSSSKIKAGAEQIKKFKTMMALNRPSEGETATLLQMFN	120	
DB	61	ELKISIFSHCCSLILGIVIGSSSKIKAGAEQIKKFKTMMALNRPSEGETATLLQMFN	120	
QY	121	PHRAIDWINGQPMWGSFVPLPLTTDPESPKERFMDQIKIVASYAQMVTYTTTIKEYLAECM	180	
DB	121	PHRAIDWINGQPMWGSFVPLPLTTDPESPKERFMDQIKIVASYAQMVTYTTTIKEYLAECM	180	
QY	181	DATLTTPV 189		
DB	181	DATLTTPV 189		
RESULT 2	VP40_BDV	STANDARD;	PRT;	370 AA.
ID	VP40_BDV			
AC	Q01552;			
DT	01-JUL-1993 (rel. 26, Created)			